



SUBSTITUTE SEQUENCE LISTING

<110> Sleeman, Matthew
Murison, Greg

<120> Fibroblast Growth Factor Receptors and Methods for Their Use

<130> 11000.1037c5

<150> U.S. 09/823,038
<151> 2001-03-28

<150> U.S. 09/383,586
<151> 1999-08-26

<150> U.S. 09/276,268
<151> 1999-03-25

<150> PCT/NZ00/00015
<151> 2000-02-18

<150> U.S. 60/221,216
<151> 2000-07-25

<150> U.S. 10/157,444
<151> 2000-05-28

<150> PCT/NZ03/00105
<151> 2003-05-27

<160> 145

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tgtgggtggc cagaagtttgc tgggtttgcc cacgggtat gtgtggtcac ggcctgtatgg 180
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ctgccttaggt gcaaatacca tgggtacag tttccgtacgc gccttcctca ctgtattacc 300
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agggtctgaa	ggtgaaggag	gtggaggccg	aggatgccgg	tgtttatgtg	tgcaaggcca	480
ccaatggctt	tggcagccctc	agcgtcaact	acactctcat	catcatggat	gatattagtc	540
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cgccccccgc	ctgatcc	tcgacgt	acgcgcctc	ttcccttgc	ctggagctc	300
gcccggaggg	ggccggacc	ctggctc	ggccgcgacc	tgggtcttgc	gggcctgagc	360
cctgagtggc	gtcc	cgttca	gctcc	accgcgc	tgcttcagg	420
agatgacgcg	gagccccgcg	ctgtgtc	tgctattgg	ggccctccc	tccggctgagg	480
cgccgcgaga	tgtatatt	ccaggg	agagcc	gccagg	tcttcgggg	540
gccaggagga	cccagcc	cagc	gtgg	cacgg	ccctcca	600
tgaggcgccg	agtatt	ccgg	gtat	gcgg	tggtggcc	660
gtgggcaccc	acggcc	atcat	tgga	tgaagg	ccagac	720
aggctagtga	acac	aga	gtgg	actg	gac	780

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ccattgtatgt	gggtggccag	aagtttgtgg	tggtgcccac	gggtgatgtg	tggtcacggc	1080
ctgatggctc	ctacactcaac	aagctgctca	tctctcggc	ccgcccaggat	gatgctggca	1140
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tattaccaga	ccccaaacct	cctccagggc	ctcctatggc	ttcttcatcg	tcatccacaa	1260
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tgcctggca	tcgtccccca	gggacatccc	gagaacgcag	tggtgacaag	gacctgccc	1440
cattggctgt	gggcatatgt	gaggagcatg	gatccgccc	ggccccccag	cacatcctgg	1500
cctctggctc	aactgctggc	cccaagctgt	accccaagct	atacacagat	gtgcacacac	1560
acacacatac	acacacactgc	actcacacgc	tctcatgtgg	agggcaaggt	tcatcaacac	1620
cagcatgtcc	actatcagtg	ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	1680
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gtgccagtgg	agggggaccc	gccgcccgtg	accatgtgga	ccaaggatgg	ccgcaccatc	240
cacagcggct	ggagccgctt	ccgcgtgctg	ccgcaggggc	tgaaggtgaa	gcaggtggag	300
cgggaggatg	ccggcgtgta	cgtgtgcaag	gccaccaacg	gcttcggcag	ccttagcg	360
aactacaccc	tcgtcgtgct	ggatgacatt	agcccaggga	aggagagcct	ggggccccac	420
agctcctctg	ggggtaaga	ggaccccgcc	agccagcagt	gggcacgacc	gwgcttcaca	480
cagccctcca	agatgaggcg	ccgggtgatc	gcacggcccg	tggtagctc	cgtgcggctc	540
aagtgcgtgg	ccagcgggca	ccctcgccc	gacatcacgt	ggtgaagga	cgaccaggcc	600
ttgacgcgc	cagaggccgc	ttagccagg	aagaagaagt	ggacactgag	cctgaagaac	660
ctgcggccgg	aggacagcgg	caaatacacc	tgccgcgtgt	cgaaccgcgc	gggcgcacatc	720
aacgcacact	acaaggtgga	tgtgatccag	cgacccgtt	ccaagcccgt	gctcacaggg	780
acgcaccccg	tgaacacgac	ggtggacttc	ggggggacca	cgtccttcca	gtgcaaggtg	840
cgcacgcacg	tgaagccggt	gatccagtgg	ctgaagcgcg	tggagtagcgg	cgccgaggc	900
cgcacacaact	ccaccatcga	tgtggccggc	cagaagttt	tggtgctgcc	cacgggtgac	960
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1								5							15							
Val									Lys													
									Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu
									20							25					30	

Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val
 35 40 45
 Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn
 50 55 60
 Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile
 65 70 75 80
 Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu
 85 90 95
 Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser
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 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg
 130 135 140
 Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val
 145 150 155 160
 Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
 165 170 175
 Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala
 180 185 190
 Ser Glu His Arg Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys
 195 200 205
 Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly
 210 215 220
 Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser
 225 230 235 240
 Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe
 245 250 255
 Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro
 260 265 270
 Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His
 275 280 285
 Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr
 290 295 300

Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu
 305 310 315 320
 Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly
 325 330 335
 Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu
 340 345 350
 Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser
 355 360 365
 Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val
 370 375 380
 Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys
 385 390 395 400
 Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro
 405 410 415
 Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala
 420 425 430
 Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile
 435 440 445
 Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr
 450 455 460
 Thr Asp Val His Thr His Thr His Thr Cys Thr His Thr Leu
 465 470 475 480
 Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val
 485 490 495
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 515 520 525
 Ser

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 35 40 45
 Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 50 55 60
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
 65 70 75 80
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
 85 90 95
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
 100 105 110
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
 115 120 125
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
 130 135 140
 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
 145 150 155 160

Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
 165 170 175
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
 180 185 190
 Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
 195 200 205
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
 210 215 220
 Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
 225 230 235 240
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
 245 250 255
 Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Pro Gly Pro Pro Met
 260 265 270
 Ala Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly
 275 280 285
 Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu
 290 295 300
 Cys Gln Thr Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val
 305 310 315 320
 Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys
 325 330 335
 Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala
 340 345 350
 Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys
 355 360 365
 Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His
 370 375 380
 Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro
 385 390 395 400
 Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys
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 Asn Asn Gly Gly Arg Val Ser
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 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110

Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140
 Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile
 145 150 155 160
 Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly
 165 170 175
 His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr
 180 185 190
 Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu
 195 200 205
 Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser
 210 215 220
 Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln
 225 230 235 240
 Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr
 245 250 255
 Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser
 260 265 270
 Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala
 275 280 285
 Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val
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 Asn Lys Pro Leu

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 <212> DNA
 <213> Mouse

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35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100 105 110	
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser	
115 120 125	
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg	
130 135 140	
Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val	
145 150 155 160	
Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro	
165 170 175	
Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala	
180 185 190	
Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys	

195	200	205
Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly		
210	215	220
Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser		
225	230	235
Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe		
245	250	255
Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro		
260	265	270
Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His		
275	280	285
Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr		
290	295	300
Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu		
305	310	315
Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly		
325	330	335
Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu		
340	345	350
Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser		
355	360	365
Thr Ser Leu Pro Trp		
370		

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 <211> 135
 <212> PRT
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<400> 14
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 Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala
 35 40 45
 Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys
 50 55 60
 Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His
 65 70 75 80
 Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro
 85 90 95
 Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys
 100 105 110
 Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu
 115 120 125
 Asn Asn Gly Gly Arg Val Ser
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<210> 15
 <211> 37
 <212> PRT
 <213> Mouse

<400> 15

Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val

1	5	10	15												
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
				20			25						30		
Pro	Asp	Gly	Ser	Tyr											
				35											

<210> 16
<211> 1515
<212> DNA
<213> Human

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gccccgctgg gccgcactgt gcccgcgtgg tgcccagtgg agggggaccc gccggccgtg	240
accatgtggc ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgtg	300
ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgtt cgtgtgcaag	360
gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgtt ggatgacatt	420
agcccaggga aggagagcct ggggcccac agctcctctg ggggtcaaga ggaccccgcc	480
agccagcagt gggcacgacc ggcgttcaca cagccctcca agatgaggcg ccgggtgtac	540
gcacggcccg tggtagctc cgtgcggctc aagtgcgtgg ccagcggca ccctcgccc	600
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aagaagaagt ggacactgag cctgaagaac ctgcggccgg aggacagcgg caaatacacc	720
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<210> 17
<211> 504
<212> PRT
<213> Human

<400> 17			
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu			
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala			
20	25	30	
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg			
35	40	45	
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr			
50	55	60	
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu			
65	70	75	80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val			
85	90	95	

Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140
 Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile
 145 150 155 160
 Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly
 165 170 175
 His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr
 180 185 190
 Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu
 195 200 205
 Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser
 210 215 220
 Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln
 225 230 235 240
 Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr
 245 250 255
 Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser
 260 265 270
 Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala
 275 280 285
 Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val
 290 295 300
 Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu
 305 310 315 320
 Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr
 325 330 335
 Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe
 340 345 350
 Leu Thr Val Leu Pro Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser
 355 360 365
 Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro
 370 375 380
 Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln
 385 390 395 400
 Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly
 405 410 415
 His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu
 420 425 430
 Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
 435 440 445
 Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
 450 455 460
 Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
 465 470 475 480
 His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
 485 490 495
 His Gln His Ile His Tyr Gln Cys
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<210> 18
 <211> 1161
 <212> DNA
 <213> Human

<400> 18

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accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggg	aggagacgtt	ggggcccgac	agctcctctg	ggggtaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccg	tggtagctc	cgtagcggctc	aagtgcgtgg	ccagcgggca	ccctcgcccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgccc	cagaggccgc	tgagccagg	600
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tgcccgctgt	cgaaaccgc	ggggccatc	aacgcacact	acaaggtgga	tgtgatccac	720
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ttactgggcc	caggcccagt	tgctggccct	aagttgtacc	ccaaactcta	cacagacatc	1080
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catatccact	atcgtgcta	g				1161

<210> 19

<211> 386
<212> PRT
<213> Human

<400> 19

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1					5					10				15

Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
					20				25				30		

Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
					35				40				45		

Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
					50				55				60		

Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
					65				70				75		80

Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
					85				90				95		

Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
					100				105				110		

Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
					115				120				125		

Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
					130				135				140		

Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile

145				150					155					160	
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly
					165				170				175		

His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr
					180				185				190		

Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu

195	200	205
Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser		
210	215	220
Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile His		
225	230	235
Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser Ser Ala Thr Ser		
245	250	255
Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile		
260	265	270
Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys		
275	280	285
Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr		
290	295	300
Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu		
305	310	315
Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala		
325	330	335
Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu		
340	345	350
Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His Ser		
355	360	365
His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His Tyr		
370	375	380
Gln Cys		
385		

<210> 20
 <211> 1230
 <212> DNA
 <213> Human

<400> 20

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cccgaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ctttagcgtc	aactacaccc	tcgtcgtgt	ggatgacatt	360
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<210> 21
 <211> 409
 <212> PRT

<213> Human

<400> 21

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
20 25 30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
35 40 45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
50 55 60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65 70 75 80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
85 90 95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
100 105 110
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
115 120 125
Pro Asp Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
130 135 140
Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
145 150 155 160
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
165 170 175
Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
180 185 190
Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
195 200 205
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
210 215 220
Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met
225 230 235 240
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
245 250 255
Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Gln Gly Pro Pro Val Ala
260 265 270
Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile
275 280 285
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys
290 295 300
Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro
305 310 315 320
Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp
325 330 335
Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys
340 345 350
Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly
355 360 365
Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His
370 375 380
Thr His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys
385 390 395 400
Val His Gln His Ile His Tyr Gln Cys
405

<210> 22

<211> 1434
<212> DNA
<213> Human

<400> 22

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tcctcgctct	cggccactag	cctggccgtgg	cccgtggtca	tcggcatccc	agccggcgct	1080
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<210> 23

<211> 477

<212> PRT

<213> Human

<400> 23

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
1					5					10				15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
					20				25				30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
					35				40			45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
					50				55			60			
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
					65				70			75			80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
					85				90			95			
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
					100				105			110			
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
					115				120			125			
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
					130				135			140			
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
					145				150			155			160
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys

165	170	175	
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr			
180	185	190	
Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys			
195	200	205	
Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr			
210	215	220	
His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln			
225	230	235	240
Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg			
245	250	255	
Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly			
260	265	270	
Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro			
275	280	285	
Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp			
290	295	300	
Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser			
305	310	315	320
Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Gln Gly			
325	330	335	
Pro Pro Val Ala Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val			
340	345	350	
Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu			
355	360	365	
Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala			
370	375	380	
Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser			
385	390	395	400
Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly			
405	410	415	
Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu			
420	425	430	
Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr			
435	440	445	
Thr Asp Ile His Thr His Thr His Ser His Thr His Ser His			
450	455	460	
Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys			
465	470	475	

<210> 24
 <211> 1242
 <212> DNA
 <213> Human

<400> 24

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ccctccaaga	tgaggcgccg	ggtgatcgca	cggccctgtgg	gtagctccgt	gcggctcaag	240
tgcgtggcca	gcgggcacccc	tcggcccgac	atcacgtgga	tgaaggacgca	ccaggccttg	300
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cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcg	accgcgcggg	cgccatcaac	420
gccacacctaca	aggtggatgt	gatccagcgg	acccgttcca	agcccgtgt	cacaggcacg	480
caccccggtga	acacgacggt	ggacttcggg	gggaccacgt	ccttccagtg	caaggtgcgc	540
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ttcctcaccg	tgctgccaga	ccaaaaaccg	caagggccac	ctgtggcctc	ctcgccctcg	840
gccactagcc	tgccgtggcc	cgtggtcatac	ggcatcccg	ccggcgctgt	tttcatctcg	900
ggcacccctgc	tcctgtggct	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgctgccc	960
cctccctgc	ctgggcacccg	cccgccccgg	acggcccgcg	accgcagcgg	agacaaggac	1020
cttcctcgt	tggccgcct	cagcgctggc	cctggtgtgg	ggctgtgtga	ggagcatggg	1080
tctccggcag	ccccccagca	cttactggc	ccaggccccag	ttgctggccc	taagttgtac	1140
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	1200
gtggaggcga	aggcccacca	gcacatccac	tatcagtgtc	ag		1242

<210> 25
<211> 413
<212> PRT
<213> Human

<400> 25
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
 20 25 30
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
 35 40 45
 Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 50 55 60
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 65 70 75 80
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 85 90 95
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
 100 105 110
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
 115 120 125
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 130 135 140
 Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr
 145 150 155 160
 His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln
 165 170 175
 Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg
 180 185 190
 Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly
 195 200 205
 Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
 210 215 220
 Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp
 225 230 235 240
 Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser
 245 250 255
 Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Gln Gly
 260 265 270
 Pro Pro Val Ala Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val
 275 280 285
 Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu
 290 295 300
 Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala
 305 310 315 320

<210> 26

<211> 876

<212> DNA

<213> Human

<400> 26

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gccccggctgg	gccgcactgt	gcccgtcgag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgttga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgtg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgt	ggatgacatt	360
agcccaggg	aggagagcct	ggggcccgac	agtcctctg	ggggtcaaga	ggaccccccc	420
agccagcagt	gggacccaaa	accgcaaggg	ccacctgtgg	ccttcctcg	ctcgcccaact	480
agcctggcgt	ggcccgtggt	catcggtatc	ccagccggcg	ctgtcttcat	cctgggcacc	540
ctgctcctgt	ggctttgcca	ggcccaagaag	aagccgtgca	ccccccgcgc	tgccccctccc	600
ctgcctgggc	accgccccgg	ggggacggcc	cgcgaccgca	gcggagacaa	ggaccttccc	660
tcgttggccg	ccctcagcgc	tggccctgg	gtggggctgt	gtgaggagca	tgggtctccg	720
gcagcccccc	agcaacttact	gggcccaggc	ccagttgt	gccctaagtt	gtaccccaaa	780
ctctacacag	acatccacac	acacacacac	acacactctc	acacacactc	acacgtggag	840
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<210> 27

<211> 291

<212> PRT

<213> Human

<400> 27

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
1				5				10				15			
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala	
		20						25				30			
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40				45				
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
		50				55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
		65				70			75				80		
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85				90				95			
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
				100				105				110			
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
				115				120				125			

```

Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
130 135 140
Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser Ser Ala Thr
145 150 155 160
Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe
165 170 175
Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro
180 185 190
Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly
195 200 205
Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala
210 215 220
Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro
225 230 235 240
Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys
245 250 255
Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His
260 265 270
Ser His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His
275 280 285
Tyr Gln Cys
290

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<210> 28
<211> 1080
<212> DNA
<213> Human

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<210> 29
<211> 359
<212> PRT
<213> Human

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<400> 29
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
      1           5           10          15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala

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20	25	30	
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg			
35	40	45	
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr			
50	55	60	
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu			
65	70	75	80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val			
85	90	95	
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr			
100	105	110	
Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met			
115	120	125	
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys			
130	135	140	
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp			
145	150	155	160
Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys			
165	170	175	
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr			
180	185	190	
Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys			
195	200	205	
Val Asp Val Ile His Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser			
210	215	220	
Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala			
225	230	235	240
Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala			
245	250	255	
Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His			
260	265	270	
Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro			
275	280	285	
Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu			
290	295	300	
His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val			
305	310	315	320
Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His			
325	330	335	
Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val His			
340	345	350	
Gln His Ile His Tyr Gln Cys			
355			

<210> 30
<211> 1149
<212> DNA
<213> Human

<400> 30
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gccccggctgg gccgcactgt gcccggctgg aggggggaccc gccggccgtg 180
accatgtggc ccaaggatgg ccgcaccatc cacagcggtt ggagccgctt ccgcgtgtg 240
ccgcaggggc tgaagggtgaa gcagggtggag cgggaggatg cccggcgtgtta cgtgtgcaag 300
gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgtt ggagcggacc 360
cgttccaacg ccgtgctcac aggcacgcac cccgtgaaca cgacgggtgga cttcgaaaa 420

accacgtcct	tccagtcaa	ggtgcgacg	gacgtgaagc	cggtgatcca	gtggctgaag	480
cgcgtggagt	acggcgccga	gggcccac	aactccacca	tcgatgtggg	cggccagaag	540
tttgcgtgc	tgcccacggg	tgacgtgtgg	tcgcggcccg	acggctccta	cctcaataag	600
ctgctcatca	cccgtgcccc	ccaggacgt	gcgggcatgt	acatctgcct	tggcgccaaac	660
accatgggc	acagcttccg	cagcgccctc	ctcaccgtgc	tgccagaccc	aaaaccgcaa	720
ggggcacctg	tggcctcctc	gtcctcgcc	actagcctgc	cgtggcccg	ggtcatcgcc	780
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aagaagccgt	gcaccccccgc	gcctgcccct	cccctgcctg	ggcaccgccc	gccggggacg	900
ccccgcacc	gcagcggaga	caaggacctt	ccctcggtgg	ccgcctctag	cgctggccct	960

ggtgtggggc	tgtgtgagga	gcatgggtct	ccggcagccc	cccagcactt	actggggccca	1020
ggcccagttg	ctggccctaa	gttgtacccc	aaactctaca	cagacatcca	cacacacaca	1080
cacacacact	ctcacacaca	ctcacacgtg	gagggcaagg	tccaccagca	catccactat	1140
cagtgttag						1149

<210> 31
<211> 382
<212> PRT
<213> Human

<400> 31

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	1	5	10	15
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala	20	25	30	
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	35	40	45	
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr		50	55	60	
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	65	70	75	80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val	85	90	95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	100	105	110	
Thr	Leu	Val	Val	Leu	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	115	120	125	
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	130	135	140	
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	145	150	155	160
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	165	170	175	
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	180	185	190	
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	195	200	205	
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	210	215	220	
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	225	230	235	240
Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	245	250	255	
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	260	265	270	
Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	275	280	285	

Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg
 290 295 300
 Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro
 305 310 315 320
 Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His
 325 330 335
 Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu
 340 345 350
 Tyr Thr Asp Ile His Thr His Thr His Ser His Thr His Ser
 355 360 365
 His Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys
 370 375 380

<210> 32

<211> 888

<212> DNA

<213> Human

<400> 32

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tcctctgggg	gtcaagagga	ccccgcgc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgagggcgcgg	ggtgatcgca	cggcccgtgg	gtagctccgt	gcggctcaag	240
tgcgtggcca	gcgggcacccc	tcggccgcac	atcacgtgg	tgaaggacgca	ccagggccttg	300
acgcgcggcag	aggccgcgtga	gcccaggaag	aagaagtgg	cactgagcct	gaagaacctg	360
cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcg	accgcgcggg	cgccatcaac	420
gccacacctaca	aggtggatgt	gatccaccca	aaaccgcaag	ggccacctgt	ggcctccctcg	480
tcctcgccca	ctagcctgccc	gtggcccggt	gtcatcgca	tcccagccgg	cgctgtcttc	540
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cctgcccctc	ccctgcctgg	gcacccgcgg	ccggggacgg	cccgcgaccc	cagcggagac	660
aaggaccttc	cctcggttggc	cgcctcagc	gctggccctg	gtgtggggct	gtgtgaggag	720
catgggtctc	cggcagcccc	ccagcactta	ctggggccag	gcccagttgc	tggccctaag	780
ttgtacccca	aactctacac	agacatccac	acacacacac	acacacactc	tcacacacac	840
tcacacgtgg	agggcaaggt	ccaccagcac	atccactatc	agtgctag		888

<210> 33

<211> 295

<212> PRT

<213> Human

<400> 33

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu						
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly						
20	25	30				
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro						
35	40	45				
Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met						
50	55	60				
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys						
65	70	75	80			
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp						
85	90	95				
Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys						
100	105	110				
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr						
115	120	125				

Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 130 135 140
 Val Asp Val Ile His Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser
 145 150 155 160
 Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala
 165 170 175
 Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala
 180 185 190
 Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His
 195 200 205
 Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro
 210 215 220
 Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu
 225 230 235 240
 His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val
 245 250 255
 Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His
 260 265 270
 Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val His
 275 280 285
 Gln His Ile His Tyr Gln Cys
 290 295

<210> 34

<211> 957

<212> DNA

<213> Human

<400> 34

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 tcctctgggg gtcaagagga cccgcacgc cagcagtggg agcggaccgc ttccaagccc 180
 gtgctcacag gcacgcaccc cgtgaacacg acgggtggact tcggggggac cacgtccttc 240
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 ggcgccgagg gccgcaccaa ctccaccatc gatgtggcg gccagaagtt tgggtgctg 360
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 cgtgcccggc aggacgtatgc gggcatgtac atctgccttgc ggcacacac catggctac 480
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 gctgtttca tcctggcgcac cctgctcctg tggcttgcc aggcccagaa gaagccgtgc 660
 accccccggc cttgccttc cctgcctggg caccggccgc cggggacggc cgcgcaccgc 720
 agcggagaca aggaccttcc ctcgttggcc gccctcagcg ctggccctgg tggggctg 780
 tgtgaggagc atgggtctcc ggcagccccc cagcaattac tggcccccagg cccagttgt 840
 ggccttaagt tgtacccaa actctacaca gacatccaca cacacacaca cacacactct 900
 cacacacact cacacgttga gggcaaggc caccacaca tccactatca gtgctag 957

<210> 35

<211> 318

<212> PRT

<213> Human

<400> 35

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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 20 25 30
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Gly Gly Gln Glu Asp Pro

35	40	45	
Ala Ser Gln Gln Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly			
50	55	60	
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe			
65	70	75	80
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys			
85	90	95	
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val			
100	105	110	
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg			
115	120	125	
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln			
130	135	140	
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr			
145	150	155	160
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Gln			
165	170	175	
Gly Pro Pro Val Ala Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro			
180	185	190	
Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu			
195	200	205	
Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro			
210	215	220	
Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg			
225	230	235	240
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro			
245	250	255	
Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His			
260	265	270	
Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu			
275	280	285	
Tyr Thr Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser			
290	295	300	
His Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys			
305	310	315	

<210> 36
 <211> 1161
 <212> DNA
 <213> Human

<400> 36

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gtgatcgac	ggcccgtggg	tagctccgtg	cggctcaagt	gcgtggccag	cggcaccct	180
cggcccgaca	tcacgtggat	gaaggacgac	caggccttga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacgtgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacctacaa	ggtggatgtg	360
atccagcgg	cccgttccaa	gcccgtgtc	acaggcacgc	accccgtgaa	cacgacggtg	420
gacttcgggg	ggaccacgtc	cttccagtgc	aagggtcgca	gcgacgtgaa	gccggtgatc	480
cagtggctga	agcgcgtgga	gtacggcgcc	gagggccgc	acaactccac	catcgatgtg	540
ggcggccaga	agtttgtggt	gctgcccacg	ggtgacgtgt	ggtcgccggcc	cgacggctcc	600
tacctcaata	agctgctcat	cacccgtgccc	cgccaggacg	atgcgggcat	gtacatctgc	660
cttggcgcca	acaccatggg	ctacagcttc	cgcagccct	tcctcacctg	gctgccagac	720
ccaaaaccgc	aaggggccacc	tgtggcctcc	tcgtccctgg	ccactagcct	gccgtggccc	780
gtggtcatcg	gcatcccagc	cggcgctgtc	ttcatctgg	gcaccctgt	cctgtggctt	840
tgccaggccc	agaagaagcc	gtgcacccccc	ctccccctgcc	tggcaccgc		900

355	360	365													
His	His	His	Ser	His	Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr
370	375	380													
Gln	Cys														
385															

<210> 38
<211> 795
<212> DNA
<213> Human

<400> 38	60					
atgacgccga	gccccctgtt	gctgctcctg	ctggccgcgc	tgctgctggg	ggccttccca	120
ccggccgccc	ccgcccggagg	ccccccaaag	atggccgaca	aggtggtccc	acggcaggtg	180
gccccggctgg	gccgcactgt	gcccggctgg	tgcccaactg	agggggaccc	gccggccgtg	240
accatgtgg	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	300
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtcaag	360
gccacccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcggt	ggacccaaaa	420
ccgcaagggc	cacctgtggc	ctcctcggtcc	tcggccacta	gcctgcgtg	gcccgtggc	480
atccggcatcc	cagccggcgc	tgtcttcatc	ctgggcaccc	tgctcctgt	gctttgccag	540
gcccagaaga	agccgtgcac	ccccgcgcct	gcccctcccc	tgccctggca	ccgcccgcg	600
gggacggccc	gcgaccgcag	cgagacaag	gaccttcct	cgttggccgc	cctcagcgct	660
ggccctgggt	tggggctgt	tgaggagcat	gggtctccgg	cagccccca	gcacttactg	720
ggcccaggcc	cagttgtgt	ccctaagtt	taccccaa	tctacacaga	catccacaca	780
cacacacaca	cacactctca	cacacactca	cacgtggagg	gcaagggtcca	ccagcacatc	795
cactatcagt	gttag					

<210> 39
<211> 264
<212> PRT
<213> Human

<400> 39															
Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1					5				10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
						20			25				30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
						35			40				45		
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
						50			55				60		
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
					65			70			75			80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
						85			90				95		
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
					100			105					110		
Thr	Leu	Val	Val	Leu	Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser
						115			120				125		
Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro
						130			135				140		
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln
						145			150				155		
Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly
						165			170				175		
His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu
						180			185				190		

Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
 195 200 205
 Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
 210 215 220
 Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
 225 230 235 240
 His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
 245 250 255
 His Gln His Ile His Tyr Gln Cys
 260

<210> 40

<211> 603

<212> DNA

<213> Human

<400> 40

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ccggccgccc	ccgcccaga	tgacattagc	ccagggaaagg	agagcctggg	gcccacagc	120
tcctctgggg	gtcaagagga	ccccgcccagc	cagcagtggg	acccaaaacc	gcaaggggcca	180
cctgtggct	cctcgtcctc	ggccactagc	ctgcccgtgc	ccgtggatcat	cgccatccca	240
gccccgcgt	tcttcatccct	gggcaccctg	ctcctgtggc	tttgccaggc	ccagaagaag	300
ccgtgcaccc	ccgcgcctgc	ccctccctg	cctgggcacc	gcccgcggg	gacggccgc	360
gaccgcagcg	gagacaagga	ccttcctcg	ttggccgccc	tcagcgctgg	ccctgggtgtg	420
gggctgtgtg	aggagcatgg	gtctccggca	gccccccagc	acttactggg	cccaggccca	480
gttgctggcc	ctaagttgt	ccccaaactc	tacacagaca	tccacacaca	cacacacaca	540
cactctcaca	cacactcaca	cgtggaggc	aaggtccacc	agcacatcca	ctatcagtgc	600
tag						603

<210> 41

<211> 200

<212> PRT

<213> Human

<400> 41

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu						
1 5 10 15						
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly						
20 25 30						
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro						
35 40 45						
Ala Ser Gln Gln Trp Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser						
50 55 60						
Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro						
65 70 75 80						
Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln						
85 90 95						
Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly						
100 105 110						
His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu						
115 120 125						
Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu						
130 135 140						
Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro						
145 150 155 160						
Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr						
165 170 175						

His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val
180						185					190				
His	Gln	His	Ile	His	Tyr	Gln	Cys								
195						200									

<210> 42

<211> 807

<212> DNA

<213> Human

<400> 42

atgacgccga	gccccctgtt	gctgctcctg	ctgcccgcgc	tgctgctggg	ggccttccca	60
ccggccgccc	ccgcccggagc	acgaccgcgc	ttcacacagc	cctccaagat	gaggccgggg	120
gtgatcgac	ggcccgtggg	tagctccgtg	cggctcaagt	gcgtggccag	cggccaccct	180
cggcccgaca	tcacgtggat	gaaggacgac	caggccctga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacacctaca	gttggatgtg	360
atccacccaa	aaccgcaagg	gccacctgtg	gcctccctcg	cctcgccac	tagcctgccc	420
tggcccggtgg	tcatcgccat	cccagccggc	gctgtcttca	tcctgggcac	cctgctcctg	480
tggctttgcc	aggcccagaa	gaagccgtgc	accccccgcgc	ctgcccctcc	cctgcctggg	540
caccgcgcgc	cggggacggc	ccgcgaccgc	agcggagaca	aggaccttcc	ctcggtggcc	600
gcctcagcg	ctggccctgg	tgtggggctg	tgtgaggagc	atgggtctcc	ggcagcccc	660
cagcacttac	tggcccccagg	cccagttgct	ggccctaagt	tgtaccccaa	actctacaca	720
gacatccaca	cacacacaca	cacacactct	cacacacact	cacacgtgga	ggcaaggtc	780
caccagcaca	tccactatca	gtgctag				807

<210> 43

<211> 268

<212> PRT

<213> Human

<400> 43

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1					5			10			15				
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr
					20			25			30				
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser
					35			40			45				
Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile
					50			55			60				
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu
					65			70			75			80	
Pro	Arg	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	
					85			90			95				
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile
					100			105			110				
Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Gln	Gly	Pro
					115			120			125				
Pro	Val	Ala	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	
					130			135			140				
Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu
					145			150			155			160	
Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro
					165			170			175				
Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly
					180			185			190				

Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val
 195 200 205
 Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu
 210 215 220
 Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr
 225 230 235 240
 Asp Ile His Thr His Thr His Ser His Thr His Ser His Val
 245 250 255
 Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys
 260 265

<210> 44

<211> 876

<212> DNA

<213> Human

<400> 44

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ccggccgccc	ccgccccaga	gcggaccgcgt	tccaagcccg	tgctcacagg	cacgcacccc	120
gtgaacacga	cggtgactt	cggggggacc	acgtccttcc	agtgcacagg	gcgcagcgac	180
gtgaagccgg	tgatccagt	gctgaagcgc	gtggagtagc	gcgcgcagg	ccgcacaaac	240
tccaccatcg	atgtggcgg	ccagaagttt	gtgggtctgc	ccacgggtga	cgtgtggtcg	300
cggcccgacg	gctcctaccc	caataagctg	ctcatcaccc	gtgcccgcga	ggacgatgcg	360
ggcatgtaca	tctgccttgg	cgccaaacacc	atgggtaca	gcttccgcag	cgccttcctc	420
accgtgtgc	cagacccaaa	accgcaaggg	ccacctgtgg	cctcctcg	ctcgccact	480
agcctgcgt	ggcccgtgt	catcgccatc	ccagccggcg	ctgtcttcat	cctgggcacc	540
ctgctcctgt	ggcttgcca	ggcccaagaag	aagccgtca	cccccgccgc	tgccccctccc	600
ctgctgggc	accggccgccc	ggggacggcc	cgcgaccgca	gcggagacaa	ggacccccc	660
tcgttggccg	ccctcagcgc	tggccctgg	gtggggctgt	gtgaggagca	tgggtctccg	720
gcagccccc	agcaacttact	gggcccagggc	ccagttgtcg	gccctaagtt	gtaccccaaa	780
ctctacacag	acatccacac	acacacacac	acacactctc	acacacactc	acacgtggag	840
ggcaaggtcc	accagcacat	ccactatcag	tgctag			876

<210> 45

<211> 291

<212> PRT

<213> Human

<400> 45

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu						
1	5	10	15			
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Glu Arg Thr Arg Ser Lys						
20	25	30				
Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly						
35	40	45				
Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val						
50	55	60				
Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn						
65	70	75	80			
Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly						
85	90	95				
Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile						
100	105	110				
Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala						
115	120	125				
Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro						

130	135	140
Asp Pro Lys Pro Gln Gly	Pro Pro Val Ala Ser	Ser Ser Ser Ala Thr
145	150	155
Ser Leu Pro Trp Pro Val Val Ile Gly	Ile Pro Ala Gly Ala Val	Phe
165	170	175
Ile Leu Gly Thr Leu Leu Leu Trp	Leu Cys Gln Ala Gln Lys	Lys Pro
180	185	190
Cys Thr Pro Ala Pro Ala Pro Pro	Leu Pro Gly His Arg Pro	Pro Gly
195	200	205
Thr Ala Arg Asp Arg Ser Gly	Asp Lys Asp Leu Pro	Ser Leu Ala Ala
210	215	220
Leu Ser Ala Gly Pro Gly Val Gly	Leu Cys Glu Glu His	Gly Ser Pro
225	230	235
Ala Ala Pro Gln His Leu Leu Gly	Pro Gly Pro Val Ala Gly	Pro Lys
245	250	255
Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His	His Thr His Thr His	His
260	265	270
Ser His Thr His Ser His Val Glu Gly	Lys Val His Gln His	Ile His
275	280	285
Tyr Gln Cys		
290		

<210> 46

<211> 522

<212> DNA

<213> Human

<400> 46

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ccggccgcgg	ccgcccggaga	cccaaaacccg	caaggccac	ctgtggcctc	ctcgccctcg	120
gccactagcc	tgccgtggcc	cgtggtcatc	ggcatcccgag	ccggcgctgt	cttcatcctg	180
ggcacccctgc	tcctgtggct	ttgccaggcc	cagaagaagc	cgtgcacccc	cgccgcctgcc	240
cctccctgc	ctgggcacccg	cccgccgggg	acggcccgcg	accgcagcgg	agacaaggac	300
cttccctcgt	tggccgcct	cagcgctggc	cctggtgtgg	ggctgtgtga	ggagcatggg	360
tctccggcag	ccccccagca	cttactgggc	ccaggcccag	ttgctggccc	taagttgtac	420
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	480
gtggagggca	aggccacca	gcacatccac	tatcagtgt	ag		522

<210> 47

<211> 173

<212> PRT

<213> Human

<400> 47

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu	Pro Pro Leu Leu		
1	5	10	15
Gly Ala Phe Pro Pro Ala Ala Ala	Arg Asp Pro Lys	Pro Gln Gly	
20	25	30	
Pro Pro Val Ala Ser Ser Ser Ala	Thr Ser Leu Pro	Trp Pro Val	
35	40	45	
Val Ile Gly Ile Pro Ala Gly	Ala Val Phe Ile	Leu Gly Thr Leu	Leu
50	55	60	
Leu Trp Leu Cys Gln Ala Gln Lys	Pro Cys Thr Pro	Ala Pro Ala	
65	70	75	80
Pro Pro Leu Pro Gly His Arg Pro	Pro Gly Thr Ala	Arg Asp Arg	Ser
85	90	95	
Gly Asp Lys Asp Leu Pro Ser Leu Ala	Ala Leu Ser Ala	Gly Pro	Gly

100	105	110
Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu		
115	120	125
Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr		
130	135	140
Thr Asp Ile His Thr His Thr His Ser His Thr His Ser His		
145	150	155
Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys		
165	170	

<210> 48
<211> 1072
<212> DNA
<213> Human

<400> 48						
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ccggccgccc	ccgccccgagg	ccccccaaag	atggcggaca	aggtggtccc	acggcaggtg	120
gccccgctgg	ccgcactgt	gcccgtcag	tgcccagtgg	agggggaccc	gcccggctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agtcctctg	ggggtaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccg	tggtagctc	cgtgcggctc	aagtgcgtgg	ccagcgggca	ccctcgcccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccgagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggccgg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgcctac	aacgcacact	acaagggtgga	tgtgatccag	720
cggaccgcgtt	ccaagcccgt	gctcacaggc	acgcaccccg	tgaacacgcac	ggtggacttc	780
ggggggacca	cgtccttcca	gtcaagggtg	cgcagcgcacg	tgaagccggt	gatccagtgg	840
ctgaagcgcg	tggagtagcgg	cgccgagggc	cgccacaact	ccaccatcga	tgtggccggc	900
cagaagtttgc	tggtagctgcc	cacgggtgac	gtgtggtcgc	ggcccgacgg	ctcctacctc	960
aataagctgc	tcatcacccg	tgcccgccag	gacgatgcgg	gcatgtacat	ctgccttggc	1020
gccaacacca	tggctacag	cttccgcagc	gccttcctca	ccgtgctgcc	ag	1072

<210> 49
<211> 357
<212> PRT
<213> Human

<400> 49			
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu			
1	5	10	15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala			
20	25	30	
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg			
35	40	45	
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr			
50	55	60	
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu			
65	70	75	80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val			
85	90	95	
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr			
100	105	110	
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly			
115	120	125	

Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140
 Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile
 145 150 155 160
 Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly
 165 170 175
 His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr
 180 185 190
 Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Trp Thr Leu Ser Leu
 195 200 205
 Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser
 210 215 220
 Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln
 225 230 235 240
 Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr
 245 250 255
 Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser
 260 265 270
 Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala
 275 280 285
 Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val
 290 295 300
 Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu
 305 310 315 320
 Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr
 325 330 335
 Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe
 340 345 350
 Leu Thr Val Leu Pro
 355

<210> 50

<211> 718

<212> DNA

<213> Human

<400> 50

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ccccggctgg	gccgcactgt	gcccgtcag	tgcccagtgg	aggggggaccc	gccggccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgttgcaag	300
gccaccaacg	gcttcggcag	ccttagcgta	aactacaccc	tcgtcggtct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agtcctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcctcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccg	tggtagctc	cgtgcggctc	aagtgcgtgg	ccagcgggca	ccctcggccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgccc	cagaggccgc	tgagcccaagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggccgg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgccatc	aacgccacct	acaagggtgga	tgtgatcc	718

<210> 51

<211> 239

<212> PRT

<213> Human

<400> 51

Met Thr Pro Ser Pro Leu Leu Leu Leu Pro Pro Leu Leu Leu

1	5	10	15												
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20						25				30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
			35						40			45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
			50						55			60			
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
			65						70			75			80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
			85						90			95			
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100						105			110			
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
			115						120			125			
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
			130						135			140			
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile
			145						150			155			160
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly
			165						170			175			
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr
			180						185			190			
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu
			195						200			205			
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser
			210						215			220			
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	
			225						230			235			

<210> 52

<211> 787

<212> DNA

<213> Human

<400> 52

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ccggccgccc	ccgccccagg	ccccccaaag	atggcggaca	agggtggccc	acggcagggtg	120
gccccggctgg	ccgcactgt	gcccgtcag	tgcccagtgg	agggggaccc	ggccggcgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgt	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccgac	agctcctctg	gggggtcaaga	ggaccccgcc	420
agccagcagt	gggagcggac	ccgttccaag	cccggtctca	caggcacgca	ccccgtgaac	480
acgacgggtgg	acttcgggggg	gaccacgtcc	ttccagtgtca	aggtgcgcag	cgacgtgaa	540
ccgggtatcc	agtggctgaa	gcgcgtggag	tacggcgcgg	agggccgcca	caactccacc	600
atcgatgtgg	gcggccagaa	gtttgtggtg	ctgcccacgg	gtgacgtgt	gtcgccgccc	660
gacggctct	acctcaataaa	gctgctcatc	acccgtgccc	gccaggacga	tgcgggcatg	720
tacatctgcc	ttggcgccaa	caccatggc	tacagcttcc	gcagcgcctt	cctcaccgtg	780
ctggccag						787

<210> 53

<211> 262

<212> PRT

<213> Human

<400> 53

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140
 Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
 145 150 155 160
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
 165 170 175
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
 180 185 190
 Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
 195 200 205
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
 210 215 220
 Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met
 225 230 235 240
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
 245 250 255
 Phe Leu Thr Val Leu Pro
 260

<210> 54

<211> 991

<212> DNA

<213> Human

<400> 54

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gccccgtgg	gccgcactgt	gcccgtgcag	tgcccagtgg	agggggaccc	gcccggctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggcacgaccg	360
cgcttcacac	agccctccaa	gatgaggcgc	cgggtgatcg	cacggcccgt	ggtagctcc	420
gtgcggctca	agtgcgtggc	cagcggcac	cctcggcccg	acatcacgtg	gatgaaggac	480
gaccaggcct	tgacgcgccc	agaggccgct	gagcccagga	agaagaagtg	gacactgagc	540
ctgaagaacc	tgccggccgga	ggacagcggc	aaatacacct	gccgcgtgta	gaaccgcgcg	600
ggcgccatca	acgccaccta	caaggtggat	gtgatccagc	ggaccggttc	caagcccggt	660
ctcacaggca	cgcacccgt	aaacacgacg	gtggacttcg	gggggaccac	gtccttccag	720
tgcaaggtgc	gcagcgtacgt	gaagccgtg	atccagtggc	tgaagcgcgt	ggagtagccg	780
gccgagggcc	gccacaactc	caccatcgat	gtggcggcc	agaagttgt	ggtgctgccc	840
acgggtgacg	tgtggtcgcg	gcccgcacggc	tcctaccta	ataagctgct	catcacccgt	900
gccccccagg	acgtgcggg	catgtacatc	tgccttggcg	ccaacaccat	gggctacagc	960

ttccgcagcg ctttcctcac cgtgctgcc a g

991

<210> 55
<211> 330
<212> PRT
<213> Human

<400> 55
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
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20 25 30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
35 40 45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
50 55 60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65 70 75 80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
85 90 95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
100 105 110
Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
115 120 125
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
130 135 140
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
145 150 155 160
Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
165 170 175
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
180 185 190
Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
195 200 205
Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr
210 215 220
His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln
225 230 235 240
Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg
245 250 255
Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly
260 265 270
Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
275 280 285
Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp
290 295 300
Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser
305 310 315 320
Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
325 330

<210> 56
<211> 799
<212> DNA
<213> Human

<400> 56

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ccggccgccc	ccgcccaga	tgacattagc	ccagggaaagg	agagcctggg	gcccacagc	120
tcctctgggg	gtcaagagga	ccccgcccagc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgagggcggc	ggtgatcgca	cggcccggtgg	gtagctccgt	gcccgtcaag	240
tgcgtggcca	gcgggcaccc	tcggccgcac	atcacgtgga	tgaaggacga	ccaggccttg	300
acgcgcccag	aggccgctga	gcccaggaag	aagaagtgg	caactgaccc	gaagaacctg	360
cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcg	accgcgcggg	cgccatcaac	420
gccacactaca	aggtggatgt	gatccagcgg	accgcgttcca	agcccgtgt	cacaggcacg	480
caccccggtga	acacgacggt	ggacttcggg	gggaccacgt	ccttccagtg	caagggtgcgc	540
agcgcacgtga	agccggtgat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	ggcgcccgag	aagtttgg	tgctgcccac	gggtgacgtg	660
tggtcgcggc	ccgacggctc	ctaccta	aagctgctca	tcacccgtgc	ccgcccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgcccag					799

<210> 57

<211> 266

<212> PRT

<213> Human

<400> 57

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	Leu
1					5				10					15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	
					20				25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	
					35				40				45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	
					50				55				60			
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	
					65				70			75		80		
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	
					85				90				95			
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	
					100				105				110			
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	
					115				120				125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	
					130				135				140			
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	
					145				150			155		160		
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	
					165				170				175			
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	
					180				185				190			
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	
					195				200				205			
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	
					210				215			220				
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	
					225				230			235		240		
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	
					245				250				255			
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro							
					260				265							

<210> 58

<211> 433
<212> DNA
<213> Human

<400> 58

atgacgccga	gccccctgtt	gctgctcctg	ctgccgcgc	tgctgctggg	ggccttccca	60
ccggccgcgg	ccgcccggagg	ccccccaaag	atggcggaca	aggtggtccc	acggcaggtg	120
gccccgtgg	ccgcactgt	gcccgtcag	tgcccagtgg	agggggaccc	ccgcccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtcgtg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcg	aactacaccc	tcgtcgtgt	ggatgacatt	360
agcccaggga	aggagagcct	ggggccgac	agtcctctg	gggtcaaga	ggaccccgcc	420
agccagcagt	ggg					433

<210> 59
<211> 144
<212> PRT
<213> Human

<400> 59

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1															15
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
															20
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
															35
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr	
															50
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
															65
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
															85
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
															100
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
															115
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
															130
															135
															140

<210> 60
<211> 637
<212> DNA
<213> Human

<400> 60

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ccggccgcgg	ccgcccggagg	ccccccaaag	atggcggaca	aggtggtccc	acggcaggtg	120
gccccgtgg	ccgcactgt	gcccgtcag	tgcccagtgg	agggggaccc	ccgcccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtcgtg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgt	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcg	aactacaccc	tcgtcgtgt	ggcacgaccg	360
cgcttcacac	agccctccaa	gatgaggcgc	cgggtgatcg	cacggcccg	ggtagctcc	420
gtcggtctca	agtgcgtggc	cagcggcac	cctcgcccc	acatcacgt	gatgaaggac	480
gaccaggcct	tgacgcgccc	agaggccgct	gagcccgag	agaagaatg	gacactgagc	540
ctgaagaacc	tgcggccgga	ggacagcggc	aaatacacct	gccgcgtgt	gaaccgcgcg	600
ggcccatca	acgccaccta	caaggtggat	gtgatcc			637

<210> 61
<211> 212
<212> PRT
<213> Human

<400> 61

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1															15
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
					20				25						30
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
					35				40						45
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr	
					50				55						60
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
					65				70						80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
					85				90						95
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
					100				105						110
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
					115				120						125
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
					130				135						140
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
					145				150						160
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
					165				170						175
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
					180				185						190
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
					195				200						205
Val	Asp	Val	Ile												
					210										

<210> 62
<211> 706
<212> DNA
<213> Human

<400> 62

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gccccgttgg	gccgcactgt	gcccgtgcag	tgcccagtgg	agggggaccc	gcccggctg	180
accatgttgg	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgtctg	240
ccgcaggggc	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgtt	cgtgtgcaag	300
gccaccaacg	gtttcggcag	ccttagcgtc	aactacaccc	tcgtcggtct	ggagcggacc	360
cgttccaaggc	ccgtgctcac	aggcacgcac	cccgtgaaca	cgacggtgaa	cttcgggggg	420
accacgttct	tccagtgc当地	ggtgcgc当地	gacgtgaagc	cggtgtatcca	gtggctgaag	480
cgcgtggagt	acggcgc当地	gggccc当地	aactccacca	tcgtatgtggg	cggccagaag	540
tttgtgtgc	tgccc当地	tgacgtgtgg	tcgc当地	acggctt当地	cctcaataag	600
ctgctcatca	cccg当地	ccaggacgat	gccc当地	acatctgc当地	tggc当地	660
accatgggct	acagcttccg	cagcgc当地	ctcaccgtgc	tgccag		706

<210> 63
<211> 235
<212> PRT

<213> Human

<400> 63

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
20 25 30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
35 40 45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
50 55 60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65 70 75 80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
85 90 95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
100 105 110
Thr Leu Val Val Leu Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
115 120 125
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
130 135 140
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
145 150 155 160
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val
165 170 175
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
180 185 190
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
195 200 205
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
210 215 220
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
225 230 235

<210> 64

<211> 445

<212> DNA

<213> Human

<400> 64

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ccggccgccc cccggccgaga tgacattagc ccagggaaagg agagcctggg gcccacacgc 120
tcctctgggg gtcaagagga ccccgccgc cagcagtggg caccgaccgc cttcacacag 180
ccctccaaga tgagggcgcgg ggtgatcgca cggccctgtgg gtagctccgt gcggctcaag 240
tgcgtggcca gcgggcaccc tcggcccgac atcacgtgga tgaaggacgca ccaggccttg 300
acgcgcaccc aggcgcgtga gcccaggaag aagaagtgg aactgacgcct gaagaacctg 360
cggccggagg acagcggcaa atacacctgc cgcgtgtcga accgcgcggg cgccatcaac 420
gccacacatac aggtggatgt gatcc 445

<210> 65

<211> 148

<212> PRT

<213> Human

<400> 65

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15

Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
 20 25 30
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
 35 40 45
 Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 50 55 60
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 65 70 75 80
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 85 90 95
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
 100 105 110
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
 115 120 125
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 130 135 140
 Val Asp Val Ile
 145

<210> 66
 <211> 514
 <212> DNA
 <213> Human

<400> 66
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 ccggccgccc cccgcccaga tgacattagc ccagggaaagg agagcctggg gcccgcacgc
 tcctctgggg gtcaagagga ccccgccagc cagcagtggg agcggacccg ttccaagccc
 gtgctcacag gcacgcaccc cgtgaacacg acggtgact tcggggggac cacgtccttc
 cagtgcagg tgcgcagcga cgtgaagccg gtgatccagt ggctgaagcg cgtggagtag
 ggcgcccagg gcccgcacaa ctccaccatc gatgtggcgc gccagaagtt tgggtgctg
 cccacgggtg acgtgtggtc gcccggcgcac ggctcctacc tcaataagct gctcatcacc
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<210> 67
 <211> 171
 <212> PRT
 <213> Human

<400> 67
 Met Thr Pro Ser Pro Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
 20 25 30
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
 35 40 45
 Ala Ser Gln Gln Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
 50 55 60
 Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
 65 70 75 80
 Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
 85 90 95
 Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val
 100 105 110
 Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
 115 120 125

Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
130						135					140				
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
145						150				155					160
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
					165				170						

<210> 68

<211> 718

<212> DNA

<213> Human

<400> 68

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cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacccataaa	ggtggatgtg	360
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gacttcgggg	ggaccacgtc	cttccagtgc	aagggtgcgc	gcgacgtgaa	gccgggtatc	480
cagtggctga	agcgcgtgga	gtacggcgc	gaggggccgc	acaactccac	catcgatgtg	540
ggcggccaga	agtttgtggt	gctgcccacg	ggtgacgtgt	ggtcgccg	cgacggctcc	600
tacctaata	agctgctcat	cacccgtgccc	cgccaggacg	atgcgggcat	gtacatctgc	660
cttqqcqcca	acaccatqqq	ctacaqcttc	cqcaqccqcc	tcctcaccq	qctqccaq	718

<210> 69

<211> 239

<212> PRT

<213> Human

<400> 69

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu
1 5 10 15

Gly Ala Phe Pro Pro Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
 20 25 30

20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45

65 70 75 80
 Pro Arg Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
 65 70 75 80

85	90	95
Asp Ser Gly Lys Tyr Thr Cys Arg Val	Ser Asn Arg Ala Gly Ala Ile	
120	125	130

100	105	110
Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro		

115 120 125
Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly

130	135	140													
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile

145 150 155 160
 Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser

165	170	175	
Thr Ile Asp Val	Gly Gly Gln Lys Phe	Val Val Leu Pro Thr	Gly Asp

	180	185	190												
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr

195	200	205
Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn		
210	215	220
Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro		
225	230	235

<210> 70
<211> 352
<212> DNA
<213> Human

<400> 70						
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gccccggctgg	gccgcactgt	gcccgtgcag	tgcccagtgg	agggggaccc	gccgcccgtg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	gg	352

<210> 71
<211> 117
<212> PRT
<213> Human

<400> 71						
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu						
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala						
20	25	30				
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg						
35	40	45				
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr						
50	55	60				
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu						
65	70	75	80			
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val						
85	90	95				
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr						
100	105	110				
Thr Leu Val Val Leu						
115						

<210> 72
<211> 160
<212> DNA
<213> Human

<400> 72						
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tcctctgggg	gtcaagagga	ccccggcagc	cagcagtggg			160
<210> 73						
<211> 53						
<212> PRT						
<213> Human						

<400> 73
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
 20 25 30
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
 35 40 45
 Ala Ser Gln Gln Trp
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<210> 74

<211> 364
 <212> DNA
 <213> Human

<400> 74
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 gtgatcgac gggccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
 cggcccgaca tcacgtggat gaaggacgac caggccttga cgccgcggcaga ggcgcgtgag 240
 cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
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 atcc 364

<210> 75

<211> 121
 <212> PRT
 <213> Human

<400> 75
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
 20 25 30
 Gln Pro Ser Lys Met Arg Arg Val Ile Ala Arg Pro Val Gly Ser
 35 40 45
 Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
 50 55 60
 Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
 65 70 75 80
 Pro Arg Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
 85 90 95
 Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
 100 105 110
 Asn Ala Thr Tyr Lys Val Asp Val Ile
 115 120

<210> 76

<211> 433
 <212> DNA
 <213> Human

<400> 76
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 gtgaacacgca cggggggacc acgtcccttc agtgcaaggt ggcgcagcgcac 180
 gtgaagccgg tgatccagtg gctgaagcgc gtggagtagc ggcgcggcacaac 240

tccaccatcg atgtggcg	ccagaagttt gtgggtgc	ccacgggtga cgtgtggc	300
cggcccgacg gctcctacct	caataagctg ctcatcaccc	gtgcccgc	360
ggcatgtaca tctgccttgg	cgccaaacacc atgggctaca	gcttccgc	420
accgtgctgc cag		cgccttc	433

<210> 77
<211> 144
<212> PRT
<213> Human

<400> 77

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu	Pro Pro Leu Leu Leu		
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Gly Ala Phe Pro Pro Ala Ala Ala	Arg Glu Arg Thr Arg Ser Lys		
20 25 30			
Pro Val Leu Thr Gly Thr His Pro Val Asn Thr	Thr Val Asp Phe Gly		
35 40 45			
Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp	Val Lys Pro Val		
50 55 60			
Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala	Glu Gly Arg His Asn		
65 70 75 80			
Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val	Leu Pro Thr Gly		
85 90 95			
Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys	Leu Leu Ile		
100 105 110			
Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile	Cys Leu Gly Ala		
115 120 125			
Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu	Thr Val Leu Pro		
130 135 140			

<210> 78
<211> 79
<212> DNA
<213> Human

<400> 78

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<210> 79
<211> 26
<212> PRT
<213> Human

<400> 79

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu	Pro Pro Leu Leu		
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Gly Ala Phe Pro Pro Ala Ala Ala	Arg		
20 25			

<210> 80
<211> 1590
<212> DNA
<213> Mouse

<400> 80

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cccaagctat	acacagatgt	gcacacacac	acacatacac	acacctgcac	tcacacgctc	1440
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<210> 81

<211> 529

<212> PRT

<213> Mouse

<400> 81

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
							20		25				30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
							35		40				45		
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
							50		55				60		
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
							65		70				75		80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
							85		90				95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
							100		105				110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
							115		120				125		
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
							130		135				140		
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
							145		150				155		160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
							165		170				175		
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
							180		185				190		

Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys
 195 200 205
 Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly
 210 215 220
 Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser
 225 230 235 240
 Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe
 245 250 255
 Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro
 260 265 270
 Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His
 275 280 285
 Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr
 290 295 300
 Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu
 305 310 315 320
 Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly
 325 330 335
 Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu
 340 345 350
 Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser
 355 360 365
 Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val
 370 375 380
 Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys
 385 390 395 400
 Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro
 405 410 415
 Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala
 420 425 430
 Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile
 435 440 445
 Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr
 450 455 460
 Thr Asp Val His Thr His Thr His Thr His Thr Cys Thr His Thr Leu
 465 470 475 480
 Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val
 485 490 495
 Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp
 500 505 510
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 515 520 525
 Ser

<210> 82
 <211> 1236
 <212> DNA
 <213> Mouse

<400> 82
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 cgcactgtgc ggctacagtg cccagtggag ggggacccac caccgttgac catgtggacc 180
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 aaggtaagg aggtggaggc cgaggatgcc ggtgtttatg ttgtcaaggc caccaatggc 300
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gcacggcctc	gcttcacaca	gcctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
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acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
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tcccgagaac	gcagtggta	caaggacctg	ccctcattgg	ctgtgggcat	atgtgaggag	960
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ctgtacccca	agctatacac	agatgtgcac	acacacacac	atacacacac	ctgcactcac	1080
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acagcgaatc	tccaagact	gtgtcctgag	gtaggcattt	gggggccaag	gcaacaggtt	1200
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<210> 83

<211> 411

<212> PRT

<213> Mouse

<400> 83

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
					20				25			30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
					35				40			45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
					50				55			60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					65				70			75			80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85				90			95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
					100				105			110			
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
					115				120			125			
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
					130				135			140			
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
					145				150			155			160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
					165				170			175			
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
					180				185			190			
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
					195				200			205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
					210				215			220			
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro
					225				230			235			240
Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Pro
					245				250			255			
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val
					260				265			270			
Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	

275	280	285	
Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly	Thr Ser Arg Glu Arg		
290	295	300	
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val	Gly Ile Cys Glu Glu		
305	310	315	320
His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser	Gly Ser Thr		
325	330	335	
Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val	His Thr His		
340	345	350	
Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys	Gly Gly Gln Gly		
355	360	365	
Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn	Thr Ala Asn Leu		
370	375	380	
Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly	Pro Arg Gln Gln Val		
385	390	395	400
Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser			
405	410		

<210> 84
 <211> 1305
 <212> DNA
 <213> Mouse

<400> 84

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aa	aa	aa	aa	aa	aa	aa	aa	aa	360
aa	aa	aa	aa	aa	aa	aa	aa	aa	365
aa	aa	aa	aa	aa	aa	aa	aa	aa	370
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tttggc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	385
tttggc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	390
tttggc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	395
tttggc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	400
tttggc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	405
tttggc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	ggcc	410

<210> 85
 <211> 434
 <212> PRT
 <213> Mouse

<400> 85

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro		
1	5	10	15												
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
20	25	30													

Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Glu Arg Thr Arg
 130 135 140
 Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp
 145 150 155 160
 Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys
 165 170 175
 Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg
 180 185 190
 His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro
 195 200 205
 Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu
 210 215 220
 Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu
 225 230 235 240
 Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val
 245 250 255
 Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser
 260 265 270
 Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala
 275 280 285
 Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys
 290 295 300
 Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro
 305 310 315 320
 Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu
 325 330 335
 Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His
 340 345 350
 Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu
 355 360 365
 Tyr Thr Asp Val His Thr His Thr His Thr Cys Thr His Thr
 370 375 380
 Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser
 385 390 395 400
 Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile
 405 410 415
 Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg
 420 425 430
 Val Ser

<210> 86
 <211> 1509
 <212> DNA

<213> Mouse

<400> 86

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gcgcgaggac	ccccaa	agaat	ggcagacaaa	gtgg	ccac	ggc	ccgc	ctgggc	120	
cgcactgtgc	ggct	acagt	cc	ca	gg	tt	gc	at	gtggacc	180
aaagatggcc	gcacaat	cca	cagt	ggct	gg	ac	cc	gt	gtgc	240
aaggtaagg	agg	tgagg	aggc	cgagg	at	gtt	ttat	tg	tgcaaggc	300
tttgcagcc	tcag	cgt	caa	ctac	act	cat	atgg	ca	ccaa	360
ccctccaaga	tgagg	gc	ccg	cgt	tg	gt	ct	gt	caag	420
tgtgtggcca	gtgg	ggc	ac	cc	ag	ac	at	cat	gtgg	480
acgcacatcg	agg	c	ct	gt	ga	ac	ca	gg	at	540
aaggctgaag	ac	at	gg	g	ca	ac	ac	gt	gg	600
gcccac	tt	gg	gg	cc	ca	ac	ac	gt	ca	660
caccctgtca	aa	gt	gg	at	gt	at	ct	ca	ac	720
agtacgtca	ac	ca	ac	ac	gg	ct	cc	ca	gg	780
cacaactcca	cc	at	tt	gt	at	gt	at	ct	ca	840
ttcctactg	tatt	acc	aga	cc	aa	ac	cc	ct	ca	1020
tccacaagcc	tg	cc	at	gg	cc	at	gg	cc	ca	1080
ggcactgtgc	tg	ct	ct	gg	ct	tg	cc	ag	gg	1140
cttccctgtgc	ct	gg	gg	ca	at	cc	ca	gt	gc	1200
ctgcccctat	tg	g	ct	gt	gg	ca	at	gg	ac	1260
atcctggcct	ct	gg	ct	ca	ac	gt	gt	ac	ag	1320
cacacacaca	ca	ca	ca	ca	ca	ca	ca	ca	ca	1380
tcaacaccag	ca	tg	cc	ac	at	ca	tg	ca	ac	1440
gaggtaggca	tt	tg	gg	gg	cc	aa	gg	ca	aa	1500
gtatcttag										1509

<210> 87

<211> 502

<212> PRT

<213> Mouse

<400> 87

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1															
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Trp	Thr	Leu	Ser	

165	170	175	
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val			
180	185	190	
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile			
195	200	205	
Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn			
210	215	220	
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg			
225	230	235	240
Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly			
245	250	255	
Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe			
260	265	270	
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr			
275	280	285	
Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met			
290	295	300	
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala			
305	310	315	320
Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala			
325	330	335	
Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile			
340	345	350	
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys			
355	360	365	
Gln Thr Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro			
370	375	380	
Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp			
385	390	395	400
Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met			
405	410	415	
Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu			
420	425	430	
Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr			
435	440	445	
Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala			
450	455	460	
Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro			
465	470	475	480
Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn			
485	490	495	
Asn Gly Gly Arg Val Ser			
500			

<210> 88
 <211> 1317
 <212> DNA
 <213> Mouse

<400> 88
 atgacgcgga gccccgcgct gctgctgctg ctattgggg ccctcccgctc ggctgaggcg 60
 gcgcgagatg atattagtcc agggaaaggag agccctgggc caggtggttc ttccgggggc 120
 caggaggacc cagccagcca gcagtggca cggcctcgct tcacacagcc ctccaaagatg 180
 aggcgcccgg tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tggccagt 240
 gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag 300
 gcttagtgaac acagaaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac 360
 agtggcaagt acacgtgccc tggatctaacc aaggccggtg ccatcaacgc cacctacaaa 420

gtggatgtaa	tccagcggac	tcgttccaag	cctgtgctca	cagggacaca	ccctgtgaac	480
acaacgggtgg	acttcgggtgg	gacaacgtcc	ttccagtgca	aggtgcgcag	tgacgtgaag	540
cctgtatcc	agtggctgaa	gccccgtggag	tacggctccg	agggacgcca	caactccacc	600
attgatgtgg	gtggccagaa	gtttgtgggt	ttgcccacgg	gtatgtgtg	gtcacggcct	660
gatggctct	acctaaca	gctgctcatc	tctcgccc	gccaggatga	tgctggcatg	720
tacatctgc	taggtgcaaa	tacatgggc	tacagttcc	gtagcgcctt	cctcaactgta	780
ttaccagacc	ccaaaccc	aggcctcct	atggcttctt	catcgatcatc	cacaagcctg	840
ccatggcctg	tggatcg	catcccagct	ggtgctgtct	tcatcctagg	cactgtgctg	900
ctctggcttt	gccagaccaa	gaagaagcca	tgtgccccag	catctacact	tcctgtgcct	960
gggcatcg	ccccagg	atcccgagaa	cgcagtgg	acaaggacct	gccctcattg	1020
gctgtggca	tatgtgagga	gcatggatcc	gccatggccc	cccagcacat	cctggcctct	1080
ggctcaactg	ctggcccaa	gctgtacccc	aagctataca	cagatgtgca	cacacacaca	1140
catacacaca	cctgactca	cacgctctca	tgtggagg	aagttcattc	aacaccagca	1200
tgtccactat	cagtctaaa	tacagcgaat	ctccaagcac	tgtgtctga	ggtaggcatt	1260
tggggccaa	ggcaacaggt	tggagaatt	gagaacaatg	gaggaagagt	atcttag	1317

<210> 89

<211> 438

<212> PRT

<213> Mouse

<400> 89

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1															
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
35															
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
50															
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65															
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
85															
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
100															
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
115															
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
130															
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145															
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
165															
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
180															
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
195															
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
210															
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225															
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
245															
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala
260															
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile

275	280	285	
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val	Leu Leu Trp Leu Cys		
290	295	300	
Gln Thr Lys Lys Pro Cys Ala Pro Ala Ser	Thr Leu Pro Val Pro		
305	310	315	320
Gly His Arg Pro Pro Gly Thr Ser Arg	Glu Arg Ser Gly Asp Lys Asp		
325	330	335	
Leu Pro Ser Leu Ala Val Gly Ile Cys	Glu Glu His Gly Ser Ala Met		
340	345	350	
Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr	Ala Gly Pro Lys Leu		
355	360	365	
Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His	His Thr His Thr His Thr		
370	375	380	
Cys Thr His Thr Leu Ser Cys Gly Gly Gln	Gly Ser Ser Thr Pro Ala		
385	390	395	400
Cys Pro Leu Ser Val Leu Asn Thr Ala Asn	Leu Gln Ala Leu Cys Pro		
405	410	415	
Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val	Gly Arg Ile Glu Asn		
420	425	430	
Asn Gly Gly Arg Val Ser			
435			

<210> 90

<211> 951

<212> DNA

<213> Mouse

<400> 90

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gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcagggtggc	ccgcctggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgcac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctcg	240
aaggtaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaaag	360
gagagccctg	ggccagggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gaccccaaac	ctccaggggcc	tcctatggct	tcttcatcg	catccacaag	cctgccatgg	480
cctgtggta	tcggcatccc	agctggtgct	gtcttcatcc	taggcactgt	gctgctctgg	540
ctttgccaga	ccaagaagaa	gccatgtgcc	ccagcatcta	cacttcctgt	gcctgggcat	600
cgtccccca	ggacatcccc	agaacgcagt	ggtgacaagg	acctgccctc	attggctgtg	660
ggcatatgtg	aggagcatgg	atccgcctg	gccccccagc	acatcctggc	ctctggctca	720
actgctggcc	ccaagctgta	ccccaaagcta	tacacagatg	tgcacacaca	cacacataca	780
cacacctgca	ctcacacgct	ctcatgtgga	gggcaagggtt	catcaacacc	agcatgtcca	840
ctatcagtgc	taaatacagc	gaatctccaa	gcactgtgtc	ctgaggtagg	catttggggg	900
ccaaggcaac	aggttggag	aattgagaac	aatggaggaa	gagtatctta	g	951

<210> 91

<211> 316

<212> PRT

<213> Mouse

<400> 91

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu	Gly Ala Leu Pro		
1	5	10	15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg	Met Ala Asp Lys Val Val		
20	25	30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg	Leu Gln Cys Pro		

35	40	45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg			
50	55	60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu			
65	70	75	80
Lys Val Lys Glu Val Ala Glu Asp Ala Gly Val Tyr Val Cys Lys			
85	90	95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile			
100	105	110	
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser			
115	120	125	
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Asp Pro Lys Pro			
130	135	140	
Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Thr Ser Leu Pro Trp			
145	150	155	160
Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr			
165	170	175	
Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala			
180	185	190	
Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu			
195	200	205	
Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu			
210	215	220	
Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser			
225	230	235	240
Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr			
245	250	255	
His Thr His Thr His Cys Thr His Thr Leu Ser Cys Gly Gly Gln			
260	265	270	
Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn			
275	280	285	
Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln			
290	295	300	
Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser			
305	310	315	

<210> 92
 <211> 1155
 <212> DNA
 <213> Mouse

<400> 92
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 cgcactgtgc ggctacagtg cccagtggag ggggacccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg 240
 aaggtaagg aggtggaggc cgaggatgcc ggtgttatg ttgtcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg cacggcctcg cttcacacag 360
 ccctccaaga tgagggcggc agtgattgca cggcctgtgg gtagctctgt gggctcaag 420
 tgtgtggcca gtgggcaccc acggccagac atcatgtgga tgaaggatga ccagacctt 480
 acgcacatcg aggctagtga acacagaaag aagaagtggc cactgagctt gaagaacctg 540
 aaggctgaag acagtggcaa gtacacgtgc cgtgtatcta acaaggccgg tgccatcaac 600
 gcccacatca aagtggatgt aatccacccc aaacctccag ggcctcttat ggcttctca 660
 tcgtcatcca caaggcctgca atggcctgtg gtgatggca tcccagctgg tgctgtctc 720
 atcctaggca ctgtgctgct ctggcttgc cagaccaaga agaagccatg tgccccagca 780
 tctacacttc ctgtgcctgg gcatcgccc ccagggacat cccgagaacg cagtgggtgac 840
 aaggacactgc cctcattggc tgtggcata tgtgaggagc atggatccgc catggccccc 900

cagcacatcc tggcctctgg ctcaactgct ggccccaaagc tgtaccccaa gctatacaca	960
gatgtgcaca cacacacaca tacacacacc tgcactcaca cgctctcatg tggagggcaa	1020
ggttcatcaa caccagcatg tccactatca gtgctaaata cagcgaatct ccaagcactg	1080
tgtcctgagg taggcatttg ggggccaagg caacaggttg ggagaattga gaacaatgga	1140
ggaagagtagt cttag	1155

<210> 93
<211> 384
<212> PRT
<213> Mouse

<400> 93	
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1 5 10 15	
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20 25 30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100 105 110	
Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val	
115 120 125	
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser	
130 135 140	
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu	
145 150 155 160	
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser	
165 170 175	
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val	
180 185 190	
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile	
195 200 205	
His Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Thr	
210 215 220	
Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe	
225 230 235 240	
Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Pro	
245 250 255	
Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly	
260 265 270	
Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val	
275 280 285	
Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu	
290 295 300	
Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr	
305 310 315 320	
Asp Val His Thr His Thr His Thr His Cys Thr His Thr Leu Ser	
325 330 335	
Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu	
340 345 350	
Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly	

355	360	365
Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly	Gly Arg Val Ser	
370	375	380

<210> 94
<211> 1224
<212> DNA
<213> Mouse

<400> 94

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cgcactgtgc ggctacagtgc cccagtggag ggggacccac caccgttgcac catgtggacc	180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggcttg	240
aaggtaagg aggtggaggc cgaggatgcc ggtgtttatg ttgtcaaggc caccaatggc	300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg agcggactcg ttccaagcct	360
gtgctcacag ggacacacccc ttgtaacaaca acgggtggact tcgggtggac aacgtccttc	420
cagtgcagg tgcgcagtga cgtgaagcct gtgatccagt ggctgaagcg ggtggagtac	480
ggctccgagg gacgccacaa ctccaccatt gatgtgggtg gccagaagtt ttgtgggttg	540
cccacgggtg atgtgtggtc acggcctgtat ggctcctacc tcaacaagct gctcatctct	600
cggggccgccc aggatgtatgc tggcatgtac atctgccttag gtgcaaatac catggctac	660
agttccgtat gcgccttcct cactgtatcca ccagacccca aacctccagg gcctcctatg	720
gcttcttcat cgtcatccac aagcctgcca tggcctgtgg tgatcggcat cccagctgg	780
gctgtcttca tcctaggcac ttgtgctgctc tggcttgc agaccaagaa gaagccatgt	840
gccccagcat ctacacttcc tgcgcctggg catcgcccc cagggacatc cccgagaacgc	900
agtggtgaca aggacctgccc ctcattggct gtggcatat gtgaggagca tggatccgccc	960
atggcccccc agcacatcct ggccctctggc tcaactgctg gccccaaagct gtaccccaag	1020
ctatacacag atgtgcacac acacacacat acacacacct gcaactcacac gctctcatgt	1080
ggagggcaag gttcatcaac accagcatgt ccactatcag tgctaaatac agcgaatctc	1140
caagcactgt gtcctgaggt aggcattgg gggccaaggc aacaggttgg gagaatttag	1200
aacaatggag gaagagatatc tttag	1224

<210> 95
<211> 407
<212> PRT
<213> Mouse

<400> 95

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	15
1 5 10	
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20 25 30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100 105 110	
Met Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val	
115 120 125	
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val	
130 135 140	
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr	

145	150	155	160												
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
165	170	175													
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
180	185	190													
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
195	200	205													
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
210	215	220													
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met
225	230	235	240												
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
245	250	255													
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu
260	265	270													
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val
275	280	285													
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys
290	295	300													
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala
305	310	315	320												
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys
325	330	335													
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His
340	345	350													
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro
355	360	365													
Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys
370	375	380													
Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu
385	390	395	400												
Asn	Asn	Gly	Gly	Arg	Val	Ser									
	405														

<210> 96

<211> 963

<212> DNA

<213> Mouse

<400> 96

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gcgcgagatg	atattagtcc	aggaaaggag	agccctgggc	caggtggttc	tgcggggggc	120
caggaggacc	cagccagcca	gcagtggca	cggcctcgct	tcacacagcc	ctccaagatg	180
aggcgccgag	tgattgcacg	gcctgtgggt	agctctgtgc	ggctcaagtg	tgtggccagt	240
gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
agtggcaagt	acacgtgccc	tgtatcta	aaggccgg	ccatcaacgc	cacccataaaa	420
gtggatgtaa	tccacccaa	acctccagg	cctcctatgg	cttcttcatc	gtcatccaca	480
agcctgccc	ggcctgtgg	gatcgccatc	ccagctgg	ctgtcttcat	cctaggcact	540
gtgctgtct	ggctttgcca	gaccaagaag	aagccatgt	ccccagc	tacacttcct	600
gtgcctggc	atcgcccc	agggacatcc	cgagaacgc	gtgggtgacaa	ggacccgtccc	660
tcattggct	tgggcatatg	tgaggagcat	ggatccgcca	tggccccc	gcacatcctg	720
gcctctggct	caactgctgg	ccccaa	tacccca	tatacacaga	tgtgcacaca	780
cacacacata	cacacac	cactcacacg	ctctcatgt	gagggcaagg	ttcatcaaca	840
ccagcatgtc	cactatc	gctaaata	gcgaatctcc	aagcactgt	tcctgaggta	900
ggcatttggg	ggccaagg	acaggttggg	agaattgaga	acaatggagg	aagagtatct	960
tag						963

<210> 97
<211> 320
<212> PRT
<213> Mouse

<400> 97

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1					5				10			15			
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
					20				25			30			
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
					35				40			45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
					50				55			60			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
					65				70			75			80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
					85				90			95			
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
					100				105			110			
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
					115				120			125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
					130				135			140			
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr
					145				150			155			160
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe
					165				170			175			
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro
					180				185			190			
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly
					195				200			205			
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val
					210				215			220			
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu
					225				230			235			240
Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr
					245				250			255			
Asp	Val	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser		
					260				265			270			
Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu
					275				280			285			
Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly
					290				295			300			
Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser
					305				310			315			320

<210> 98
<211> 1032
<212> DNA
<213> Mouse

<400> 98

atgacgcgga	cccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctgggc	caggtggttc	ttcggggggc	120
caggaggacc	cagccagcca	gcagtgggag	cggactcggt	ccaagcctgt	gctcacaggg	180

acacaccctg	tgaacacaac	ggtggacttc	ggtggacaa	cgtccttcca	gtgcaaggtg	240
cgcagtgacg	tgaaggctgt	gatccagtgg	ctgaagcggg	tggagtagcgg	ctccgaggga	300
cgcacaact	ccaccattga	tgtgggtggc	cagaagttt	tgggtgtgcc	cacgggtgat	360
gtgtggtcac	ggcctgatgg	ctcc tacctc	aacaagctgc	tcatctctcg	ggcccgccag	420
gatgatgctg	gcatgtacat	ctgcctaggt	gcaaatacca	tgggctacag	tttccgttagc	480
gccttcctca	ctgtattacc	agaccccaa	cctccaggc	ctcctatggc	ttcttcatcg	540
tcatccacaa	gcctgccatg	gcctgtggt	atcggcatcc	cagctggtgc	tgtcttcatc	600
ctagggactg	tgctgctctg	gcttgccag	accaagaaga	agccatgtgc	cccagcatct	660
acacttcctg	tgccctggca	tcgtccccca	gggacatccc	gagaacgcag	tggtacaag	720
gacctgcct	cattggctgt	gggcataatgt	gaggagcatg	gatccgcct	ggccccccag	780
cacatcctgg	cctctggctc	aactgctggc	cccaagctgt	accccaagct	atacacagat	840
gtgcacacac	acacacatac	acacacctgc	actcacacgc	tctcatgtgg	agggcaaggt	900
tcatcaacac	cagcatgtcc	actatcagtg	ctaaatacag	cgaatctcca	agcactgtgt	960
cctgaggtag	gcattttgggg	gccaggcaaa	caggttggga	gaattgagaa	caatggagga	1020
agagtatctt	ag					1032

<210> 99

<211> 343

<212> PRT

<213> Mouse

<400> 99

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro		
1					5				10			15				
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	
					20				25			30				
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	
					35			40			45					
Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	
					50			55			60					
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	
					65			70			75			80		
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	
					85			90			95					
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	
					100			105			110					
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	
					115			120			125					
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	
					130			135			140					
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	
					145			150			155			160		
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	
					165			170			175					
Ala	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
					180			185			190					
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	
					195			200			205					
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	
					210			215			220					
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	
					225			230			235			240		
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	
					245			250			255					
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	
					260			265			270					
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	

275	280	285
Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro		
290	295	300
Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys		
305	310	315
Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu		
325	330	335
Asn Asn Gly Gly Arg Val Ser		
340		

<210> 100
<211> 1236
<212> DNA
<213> Mouse

<400> 100	60
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gcgcgagcac ggcctcgctt cacacagccc tccaagatga ggcgcgcgagt gattgcacgg	180
cctgtggta gctctgtcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc	240
atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag	300
aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt	360
gtatctaaca aggccgggtgc catcaacgccc acctacaaag tggatgtaat ccagcggact	420
cgttccaagc ctgtgctcac agggacacac cctgtgaaca caacggtgga cttcggtggg	480
acaacgtcct tccagtgcaa ggtgcgcagt gacgtgaagc ctgtgatcca gtggctgaag	540
cgggtggagt acggctccga gggacgccc aactccacca ttgatgtggg tggccagaag	600
tttgggtgt tgcccacggg tggatgtgtgg tcacggcctg atggctccta cctcaacaag	660
ctgctcatct ctcggggcccg ccaggatgtat gctggcatgt acatctgcct aggtgcaaat	720
accatgggct acagtttccg taggccttc ctcactgtat taccagaccc caaacctcca	780
gggcctccta tggcttc ttc atcgtcatcc acaaggctgc catggcctgt ggtgatcgcc	840
atcccagctg gtgctgtctt catcctaggc actgtgctgc tctggcttt ccagaccaag	900
aagaagccat gtgcccagc atctacactt cctgtgcctg ggcacatgtcc cccagggaca	960
tcccggaaac gcagtggta caaggacctg ccctcattgg ctgtggcat atgtgaggag	1020
catggatccg ccatggccccc ccagcacatc ctggcctctg gctcaactgc tggccccaag	1080
ctgtacccca agctatacac agatgtgcac acacacacac atacacacac ctgcactcac	1140
acgctctcat gtggagggca aggttcatca acaccagcat gtccactatc agtgctaaat	1200
acagcgaatc tccaagact gtgtcctgag gttaggattt gggggccaag gcaacaggtt	1236
gggagaattt agaacaatgg aggaagagta tcttag	

<210> 101
<211> 411
<212> PRT
<213> Mouse

<400> 101	15
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1 5 10 15	
Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys	
20 25 30	
Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu	
35 40 45	
Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys	
50 55 60	
Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys	
65 70 75 80	
Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys	
85 90 95	
Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr	

100	105	110
Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly		
115	120	125
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe		
130	135	140
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys		
145	150	155
Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val		
165	170	175
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg		
180	185	190
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln		
195	200	205
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr		
210	215	220
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro		
225	230	235
Gly Pro Pro Met Ala Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro		
245	250	255
Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val		
260	265	270
Leu Leu Trp Leu Cys Gln Thr Lys Lys Pro Cys Ala Pro Ala Ser		
275	280	285
Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg		
290	295	300
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu		
305	310	315
His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr		
325	330	335
Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His		
340	345	350
Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly		
355	360	365
Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu		
370	375	380
Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val		
385	390	395
Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser		
405	410	

<210> 102
 <211> 870
 <212> DNA
 <213> Mouse

<400> 102	
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gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc cgcctggc	120
cgcactgtgc ggctacagtg cccagtggag ggggaccac caccgttgc acatgtggacc	180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctcg	240
aaggtaagg aggtggaggc cgaggatgcc ggtgttatg tttgtcaaggc caccaatggc	300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg accccaaacc tccagggcct	360
cctatggctt cttccatcgtc atccacaagc ctgccatggc ctgtggatcg cggcatccca	420
gctggtgctg tcttcatcctt aggcaactgtg ctgtctggc tttggccagac caagaagaag	480
ccatgtgccc cagcatctac acttcctgtg cctggcattc gtccccccagg gacatcccga	540
gaacgcagtg gtgacaagga cctgccccta ttggctgtgg gcatatgtga ggagcatgga	600
tccgccatgg ccccccagca catcctggcc tctggctcaa ctgctggccc caagctgtac	660

cccaagctat acacagatgt gcacacacac acacatacac acacctgcac tcacacgctc	720
tcatgtggag ggcaagggttc atcaacacca gcatgtccac tatacggtct aaatacagcg	780
aatctccaag cactgtgtcc tgaggtaggc atttggggc caaggcaaca ggttgggaga	840
attgagaaca atggaggaag agtatcttag	870

<210> 103
<211> 289
<212> PRT
<213> Mouse

<400> 103	
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1 5 10 15	
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20 25 30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile	
100 105 110	
Met Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser	
115 120 125	
Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val	
130 135 140	
Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys	
145 150 155 160	
Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro	
165 170 175	
Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala	
180 185 190	
Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile	
195 200 205	
Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr	
210 215 220	
Thr Asp Val His Thr His Thr His Thr Cys Thr His Thr Leu	
225 230 235 240	
Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val	
245 250 255	
Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp	
260 265 270	
Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val	
275 280 285	
Ser	

<210> 104
<211> 678
<212> DNA
<213> Mouse

<400> 104	
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caggaggacc cagccagcca	gcagtggac	cccaaaccctc	cagggcctcc	tatggcttct	180
tcatcgcat ccacaagcct	gccatggcct	gtggtgatcg	gatcccagc	tggtgctgtc	240
ttcatcctag gcactgtgt	gctctggctt	tgccagacca	agaagaagcc	atgtgcccc	300
gcatctacac ttccctgtgcc	tgggcatcgt	cccccaggga	catcccgaga	acgcagtgg	360
gacaaggacc tgccctcatt	ggctgtggc	atatgtgagg	agcatggatc	cgccatggcc	420
ccccagcaca tcctggcctc	tggctcaact	gctggccca	agctgtaccc	caagctatac	480
acagatgtgc acacacacac	acatacacac	acctgcactc	acacgctctc	atgtggaggg	540
caaggttcat caacaccagc	atgtccacta	tcagtgctaa	atacagcgaa	tctccaagca	600
ctgtgtcctg aggtaggcat	ttgggggcca	aggcaacagg	ttgggagaat	tgagaacaat	660
ggaggaagag tatcttag					678

<210> 105

<211> 225

<212> PRT

<213> Mouse

<400> 105

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro				
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Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro				
20	25	30		
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln				
35	40	45		
Trp Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser				
50	55	60		
Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val				
65	70	75	80	
Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys				
85	90	95		
Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro				
100	105	110		
Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala				
115	120	125		
Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile				
130	135	140		
Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr				
145	150	155	160	
Thr Asp Val His Thr His Thr His Thr Cys Thr His Thr Leu				
165	170	175		
Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val				
180	185	190		
Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp				
195	200	205		
Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val				
210	215	220		
Ser				
225				

<210> 106

<211> 882

<212> DNA

<213> Mouse

<400> 106

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccgtc	ggctgaggcg	60
gcgcgagcac	ggcctcgctt	cacacagccc	tccaagatga	ggcgccgagt	gattgcacgg	120

cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagtg	ggcacccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgcacg	catctagagg	ctagtaaca	cagaaagaag	240
aagtggacac	ttagctgaa	gaacctgaaag	cctgaaagaca	gtggcaagta	cacgtccgt	300
gtatctaaca	aggccggtgc	catcaacgc	acctacaaaag	tggatgtaat	ccaccccaa	360
cctccagggc	ctcctatggc	ttcttcatcg	tcatccacaa	gcctgccatg	gcctgtggtg	420
atcggcatcc	cagctggtgc	tgtcttcatc	ctaggcactg	tgctgctctg	gctttgccag	480
accaagaaga	agccatgtgc	cccagcatct	acacttcctg	tgccctggca	tgtccccca	540
gggacatccc	gagaacgcag	tggtgacaag	gacctgcct	cattggctgt	gggcataatgt	600
gaggagcatg	gatccgccat	ggccccccag	cacatcctgg	cctctggctc	aactgctggc	660
cccaagctgt	accccaagct	atacacagat	gtgcacacac	acacacatac	acacacactgc	720
actcacacgc	tctcatgtgg	agggcaaggt	tcatcaacac	cagcatgtcc	actatcagtg	780
ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	gcatttgggg	gc当地ggcaa	840
caggttggga	gaattgagaa	caatggagga	agagtatctt	ag		882

<210> 107
<211> 293
<212> PRT
<213> Mouse

<400> 107
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile His Pro Lys Pro Pro Gly Pro Pro Met Ala Ser
 115 120 125
 Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro
 130 135 140
 Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln
 145 150 155 160
 Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly
 165 170 175
 His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu
 180 185 190
 Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala
 195 200 205
 Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr
 210 215 220
 Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr Cys
 225 230 235 240
 Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys
 245 250 255
 Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu
 260 265 270
 Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn
 275 280 285
 Gly Gly Arg Val Ser

<210> 108
 <211> 951
 <212> DNA
 <213> Mouse

<400> 108

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccg	tc ggctgaggcg	60
g	g	g	g	g	g	120
gcgcgagagc	ggactcg	ttc	caagc	cac	acc	180
gtggacttcg	gtgg	gaca	gtc	caag	gtc	240
atccagtggc	tga	gggt	ggat	ccg	gac	300
gtgggtggcc	aga	agtt	gtt	ggcc	ggat	360
tcctaccta	aca	agct	cat	ctcg	gtt	420
tgcctaggtg	caa	ataccat	gg	ctac	gtt	480
gacccaaac	ctcc	cagg	tc	tatgg	cat	540
cctgtgtga	tcgg	cat	tc	ttcat	cg	600
cttgc	ca	aga	g	gg	gt	660
cgtcccc	gg	acat	cc	gt	ctgt	720
ggcatatgt	agg	ag	atcc	gg	gt	780
actgctggcc	cca	agct	cc	ca	ccat	840
cacac	ctc	acac	ct	cat	gtt	900
ctatcagtgc	taa	atac	ac	ga	atgtt	951
ccaaggcaac	agg	ttgg	g	at	ggagg	

<210> 109
 <211> 316
 <212> PRT
 <213> Mouse

<400> 109

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1															
Ser	Ala	Glu	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr
Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser
35															
Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu
50															
Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp
65															
Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser
Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg
100															
Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
115															
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro
130															
Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	
145															
Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr
165															
Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala
180															
Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu

195	200	205
Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu		
210	215	220
Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser		
225	230	235
Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr		240
245	250	255
His Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln		
260	265	270
Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn		
275	280	285
Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln		
290	295	300
Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser		
305	310	315

<210> 110

<211> 597

<212> DNA

<213> Mouse

<400> 110

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcqagacc	ccaaacctcc	agggcctcct	atggcttctt	catcgatcatc	cacaagcctg	120
ccatggcctg	ttgtgatcgg	catcccagct	ggtgctgtct	tcatcctagg	cactgtgctg	180
ctctggcttt	gccagaccaa	gaagaagccaa	tgtgccccag	catctacact	tcctgtgcct	240
gggcatcgtc	ccccaggggac	atcccgagaa	cgcagtggtg	acaaggacct	gccctcattg	300
gctgtgggca	tatgtgagga	gcatggatcc	gccatggccc	cccagcacat	cctggcctct	360
ggctcaactg	ctggcccaa	gctgtacccc	aagctataca	cagatgtgca	cacacacaca	420
catacacaca	cctgcaactca	cacgctctca	tgtggagggc	aaggttcatc	aacaccagca	480
tgtccactat	cagtgctaaa	tacagcgaat	ctccaagcac	tgtgtcctga	ggttaggcatt	540
tggggccaa	ggcaacaggt	tggagaatt	gagaacaatg	gaggaagagt	atcttag	597

<210> 111

<211> 198

<212> PRT

<213> Mouse

<400> 111

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro			
1	5	10	15
Ser Ala Glu Ala Ala Arg Asp Pro Lys Pro Pro Gly Pro Pro Met Ala			
20	25	30	
Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile			
35	40	45	
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys			
50	55	60	
Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro			
65	70	75	80
Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp			
85	90	95	
Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met			
100	105	110	
Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu			
115	120	125	
Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr			

130	135	140
Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly	Ser Ser Thr Pro Ala	
145	150	155
Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro		160
165	170	175
Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn		
180	185	190
Asn Gly Gly Arg Val Ser		
195		

<210> 112
<211> 1060
<212> DNA
<213> Mouse

<400> 112		
atgacgcgga gccccgcgct gctgctgctg ctattgggg ccctcccgct ggctgaggcg		60
gcgcgaggac ccccaagaat ggcagacaaa gtggtcccac ggcaggtggc ccgcctggc		120
cgcactgtgc ggctacagtg cccagtggag ggggacccac caccgttgcac catgtggacc		180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggcttg		240
aaggtaagg aggtggaggc cgaggatgcc ggtgtttatg tttgcaaggc caccaatggc		300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccagggaaag		360
gagagccctg ggccagggtgg ttcttcgggg ggccaggagg accccagccag ccagcagtgg		420
gcacggcctc gcttcacaca gcctccaag atgaggcgcg gagtgattgc acggcctgtg		480
ggtagctctg tgccgctcaa gtgtgtggcc agtgggcacc cacggccaga catcatgtgg		540
atgaaggatg accagacattt gacgcata gaggcttagt aacacagaaa gaagaagtgg		600
acactgagct tgaagaacctt gaagcctgaa gacagtggca agtacacgtg ccgtgtatct		660
aacaaggccg gtgccatcaa cggccacctac aaagtggatg taatccagcg gactcgttcc		720
aaggctgtgc tcacaggac acaccctgtg aacacaacgg tggacttcgg tggacaacg		780
tccttcagg tcaagggtcg cagtgcgtg aagcctgtga tccagtggct gaagcgggtg		840
gagtaaggct cggaggacg ccacaactcc accattgtatg tgggtggcca gaagtttgg		900
gtgttggcca cgggtatgt gtggtcacgg cctgatggct cctacctcaa caagctgctc		960
atctctcgaa cccgcccagga tggatgtggc atgtacatct gcctaggtgc aaataccatg		1020
ggctacagtt tccgtacgcg ctccctcaact gtattaccag		1060

<210> 113
<211> 353
<212> PRT
<213> Mouse

<400> 113		
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro		
1 5 10 15		
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val		
20 25 30		
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro		
35 40 45		
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg		
50 55 60		
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu		
65 70 75 80		
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys		
85 90 95		
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile		
100 105 110		
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Ser		
115 120 125		

Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg
 130 135 140
 Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val
 145 150 155 160
 Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
 165 170 175
 Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala
 180 185 190
 Ser Glu His Arg Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys
 195 200 205
 Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly
 210 215 220
 Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser
 225 230 235 240
 Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe
 245 250 255
 Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro
 260 265 270
 Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His
 275 280 285
 Asn Ser Thr Ile Asp Val Gly Gln Lys Phe Val Val Leu Pro Thr
 290 295 300
 Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu
 305 310 315 320
 Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly
 325 330 335
 Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu
 340 345 350
 Pro

<210> 114
 <211> 706
 <212> DNA
 <213> Mouse

<400> 114
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgctc ggctgaggcg 60
 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctggc 120
 cgcactgtgc ggctacagtgc cccagtggag ggggacccac caccgttgcac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctcg 240
 aaggtaagg aggtggaggc cgaggatgcc ggtgtttatg ttgtcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccagggaaag 360
 gagagccctg ggcgcagggtgg ttcttcgggg ggcgcaggagg accccagccag ccagcagtgg 420
 gcacggccctc gcttcacaca gcccctccaag atgaggcgcc gagtgattgc acggcctgtg 480
 ggtagctctg tgcggctcaa gtgtgtggcc agtgggcacc cacggccaga catcatgtgg 540
 atgaaggatg accagacattt gacgcattca gaggcttagtg aacacagaaa gaagaagtgg 600
 acactgagct tgaagaacctt gaagcctgaa gacagtggca agtacacgtg ccgtgttatct 660
 aacaaggccg gtgccatcaa cgccacctac aaagtggatg taatcc 706

<210> 115
 <211> 235
 <212> PRT
 <213> Mouse

<400> 115
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro

1	5	10	15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val			
20	25	30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro			
35	40	45	
Val Glu Gly Asp Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg			
50	55	60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu			
65	70	75	80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys			
85	90	95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile			
100	105	110	
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Ser			
115	120	125	

Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg			
130	135	140	
Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val			
145	150	155	160
Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro			
165	170	175	
Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala			
180	185	190	
Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys			
195	200	205	
Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly			
210	215	220	
Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile			
225	230	235	

<210> 116

<211> 775

<212> DNA

<213> Mouse

<400> 116

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtccac	ggcaggtggc	ccgcctggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtaagg	aggtgtggagc	cgaggatgcc	ggtgtttatg	tgtcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaaag	360
gagagccctg	ggccagggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gagcggactc	gttccaagcc	tgtgctcaca	gggacacacc	ctgtgaacac	aacgggtggac	480
ttcggtggga	caacgtcctt	ccagtgcag	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
tggctgaagc	gggtggagta	cggctccgag	ggacgcccaca	actccaccat	tgatgtgggt	600
ggccagaagt	ttgtgggttt	gcccacgggt	gatgtgtgg	cacggcctga	tggctcctac	660
ctcaacaagc	tgctcatctc	tcgggccccgc	caggatgtg	ctggcatgt	catctgccta	720
ggtgcaaata	ccatgggcta	cagttccgt	agcgccttcc	tcactgtatt	accag	775

<210> 117

<211> 258

<212> PRT

<213> Mouse

<400> 117

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Glu Arg Thr Arg
 130 135 140
 Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp
 145 150 155 160
 Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys
 165 170 175
 Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg
 180 185 190
 His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro
 195 200 205
 Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu
 210 215 220
 Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu
 225 230 235 240
 Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val
 245 250 255
 Leu Pro

<210> 118
 <211> 979
 <212> DNA
 <213> Mouse

<400> 118

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccg	tc ggctgaggcg	60
g cgc gaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcagggtggc	ccgcctggc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcatctag	aggctagtga	acacagaaag	aagaagtgg	cactgagctt	gaagaacctg	540
aaggcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccagcgg	actcggttcca	agcctgtgct	cacagggaca	660
caccctgtga	acacaacggt	ggacttcgg	gggacaacgt	ccttccagtg	caagggtgcgc	720
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgaggggacgc	780
cacaactcca	ccattgtatgt	gggtggccag	aagtttgg	tgttgccac	gggtgatgtg	840
tggtcacggc	ctgatggctc	ctacactcaac	aagctgctca	tctctcg	ccgcccaggat	900

gatgctggca tgtacatctg cctaggtgca aataccatgg gctacagttt ccgtacgccc 960
ttcctcactg tattaccag 979

<210> 119
<211> 326
<212> PRT
<213> Mouse

<400> 119

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro			
1					5				10				15				
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val		
					20				25				30				
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro		
					35				40				45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg		
	50				55					60							
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu		
	65					70				75				80			
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys		
					85				90				95				
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile		
							100		105				110				
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val		
	115					120					125						
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser		
	130					135				140							
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu		
	145					150				155				160			
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser		
						165			170				175				
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val		
						180			185				190				
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile		
						195			200				205				
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn		
	210					215				220							
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg		
	225					230				235				240			
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly		
						245			250				255				
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe		
						260			265				270				
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr		
						275			280				285				
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met		
						290			295				300				
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala		
	305					310				315				320			
Phe	Leu	Thr	Val	Leu	Pro												
					325												

<210> 120
<211> 787
<212> DNA
<213> Mouse

<400> 120

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccgtc	ggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctggc	caggtggttc	ttcggggggc	120
caggaggacc	cagccagcca	gcagtggca	cggcctcgct	tcacacagcc	ctccaagatg	180
aggcgccag	tgattgcacg	gcctgtgggt	agctctgtc	ggctcaagtg	tgtggccagt	240
gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
gctagtgaac	acagaaaagaa	gaagtggaca	ctgagctta	agaacctgaa	gcctgaagac	360
agtggcaagt	acacgtgccg	tgtatcta	aaggccgg	ccatcaacgc	cacctacaaa	420
gtggatgtaa	tccagcggac	tcgttccaag	cctgtgtca	cagggacaca	ccctgtgaac	480
acaacggtgg	acttcggtgg	gacaacgtcc	ttccagtgca	aggtgcgcag	tgacgtgaag	540
cctgtgtatcc	agtggctgaa	gccccgtggag	tacggctccg	agggacgcca	caactccacc	600
atggatgtgg	gtggccagaa	gtttgtgggt	ttgcccacgg	gtgatgtgtg	gtcacggcct	660
gatggctct	acctcaacaa	gctgctcatc	tctcggcc	gccaggatga	tgctggcatg	720
tacatctgcc	taggtgcaaa	taccatgggc	tacagttcc	gtagcgcctt	cctcactgt	780
ttaccag						787

<210> 121

<211> 262
<212> PRT
<213> Mouse

<400> 121

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1						5						10		15	
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
								20				25		30	
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
								35				40		45	
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
								50			55		60		
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
								65		70		75		80	
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
								85		90		95			
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Trp	Thr	Leu	Ser	
								100		105		110			
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
								115		120		125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
								130		135		140			
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
								145		150		155		160	
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
								165		170		175			
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
								180		185		190			
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
								195		200		205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
								210		215		220			
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
								225		230		235		240	
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
								245		250		255			
Phe	Leu	Thr	Val	Leu	Pro										
						260									

<210> 122
<211> 421
<212> DNA
<213> Mouse

<400> 122

atgacgcgga	cccccgcgct	gctgctgctg	ctattggggg	ccctcccgctc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgcac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggcttg	240
aaggtaagg	aggtggaggc	cgaggatgcc	ggtgttatg	tgtcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
g						421

<210> 123
<211> 140
<212> PRT
<213> Mouse

<400> 123

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro			
1														15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val		
														20	25	30	
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro		
														35	40	45	
Val	Glu	Gly	Asp	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg			
														50	55	60	
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu		
														65	70	75	80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys		
														85	90	95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile		
														100	105	110	
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser		
														115	120	125	
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp						
														130	135	140	

<210> 124
<211> 625
<212> DNA
<213> Mouse

<400> 124

atgacgcgga	cccccgcgct	gctgctgctg	ctattggggg	ccctcccgctc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgcac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggcttg	240
aaggtaagg	aggtggaggc	cgaggatgcc	ggtgttatg	tgtcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	ttcacacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcacatctag	aggctagtga	acacagaaag	aagaagtgg	cactgagctt	gaagaacctg	540
aaggcctgaag	acagtggcaa	gtacacgtgc	cgtgttatcta	acaaggccgg	tgccatcaac	600

gccacctaca aagtggatgt aatcc

625

<210> 125
<211> 208
<212> PRT
<213> Mouse

<400> 125
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110
Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
115 120 125
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
130 135 140
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
145 150 155 160
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
165 170 175
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
180 185 190
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
195 200 205

<210> 126
<211> 694
<212> DNA
<213> Mouse

<400> 126
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgctc ggctgaggcg 60
gcgcgaggac ccccaagaat ggcagacaaa gtggtcccac ggcaggtggc cccgcctggc 120
cgcaactgtgc ggctacagtg cccagtggag ggggaccac caccgttgcac catgtggacc 180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctcg 240
aaggtaagg aggtggaggc cgaggatgcc ggtgtttatg ttgtcaaggc caccaatggc 300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg agcggactcg ttccaagcct 360
gtgctcacag ggacacaccc tgtgaacaca acgggtggact tcgggtggac aacgtccttc 420
cagtgcagg tgcgcagtga cgtgaagcct gtgatccagt ggctgaagcg ggtggagttac 480
ggctccgagg gacgccacaa ctccaccatt gatgtgggtg gccagaagtt ttgtggttg 540
cccacgggtg atgtgtggtc acggcctgat ggctccctacc tcaacaagct gctcatctc 600
cgggcccgcc aggatgtatgc tggcatgtac atctgcctag gtgcaaatac catggctac 660
agttccgta gcgccttcactgtatcca 694

<210> 127
<211> 231
<212> PRT

<213> Mouse

<400> 127

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110
Met Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val
115 120 125
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
130 135 140
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr
145 150 155 160
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys
165 170 175
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser
180 185 190
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly
195 200 205
Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
210 215 220
Ala Phe Leu Thr Val Leu Pro
225 230

<210> 128

<211> 433

<212> DNA

<213> Mouse

<400> 128

atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgct ggctgaggcg 60
gcgcgagatg atattagtcc aggaaaggag agccctgggc caggtggttc ttggggggc 120
caggaggacc cagccagcca gcagtggca cggcctcgct tcacacagcc ctccaaagatg 180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt 240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag 300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac 360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa 420
gtggatgtaa tcc 433

<210> 129

<211> 144

<212> PRT

<213> Mouse

<400> 129

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15

Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
20								25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
35								40					45		
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
50								55				60			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65								70			75		80		
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
85									90				95		
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
100								105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
115								120				125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
130								135				140			

<210> 130

<211> 502

<212> DNA

<213> Mouse

<400> 130

atgacgcgga	ccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctggc	cagggtgttc	ttcgggggc	120
caggaggacc	cagccagcca	gcagtggag	cgactcggt	ccaagcctgt	gctcacaggg	180
acacaccctg	tgaacacaac	ggtggacttc	ggtgggacaa	cgtccttcca	gtgcaaggtg	240
cgcagtgacg	tgaaggctgt	gatccagtgg	ctgaagcggg	tggagtacgg	ctccgaggga	300
cgcacacaact	ccaccattga	tgtgggtggc	cagaagtttgc	ttgtgttgc	cacgggtgat	360
gtgtggtcac	ggcctgatgg	ctccctacctc	aacaagctgc	tcatctctcg	ggccgcag	420
gatgatgctg	gcatgtacat	ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	480
gccttcctca	ctgtattacc	ag				502

<210> 131

<211> 167

<212> PRT

<213> Mouse

<400> 131

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1						5		10			15				
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
20								25				30			
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
35								40				45			
Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
50								55				60			
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
65								70			75		80		
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr
85								90				95			
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
100								105				110			
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
115								120				125			
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
130								135				140			

Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
 145 150 155 160
 Ala Phe Leu Thr Val Leu Pro
 165

<210> 132

<211> 706

<212> DNA

<213> Mouse

<400> 132

atgacgcgga	gccccgcgct	gctgctgctg	ctattgggg	ccctcccgtc	ggctgaggcg	60
gcgcgagcac	ggcctcgctt	cacacagccc	tccaagatga	ggcgccgagt	gattgcacgg	120
cctgtggta	gctctgtcg	gctcaagtgt	gtggccagtg	ggcacccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaaagaag	240
aagtggacac	tgagcttcaa	gaaccttgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccgggtgc	catcaacgac	acctacaaag	tggatgtaat	ccagcggact	360
cgttccaagg	ctgtgctcac	agggacacac	cctgtgaaca	caacggtgga	cttcgggtggg	420
acaacgtcct	tccagtgcaa	ggtgcgcagt	gacgtgaagc	ctgtgatcca	gtggctgaag	480
cgggtggagt	acggctccga	gggacgcccac	aactccacca	ttgatgtggg	tggccagaag	540
tttgtggtgt	tgcccacggg	tgtatgtgtgg	tcacggcctg	atggctccta	cctcaacaag	600
ctgctcatct	ctcgggccccg	ccaggatgtat	gctggcatgt	acatctgcct	aggtgcaaat	660
accatgggct	acagtttccg	taggccttc	ctcaactgtat	taccag		706

<210> 133

<211> 235

<212> PRT

<213> Mouse

<400> 133

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1															15
Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
															30
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu
															45
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys
															60
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys
															80
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys
															95
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr
															110
Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly
															125
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe
															140
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys
															160
Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
															175
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
															190
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln
															205

Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr

210 215 220

Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro

225 230 235

<210> 134

<211> 340

<212> DNA

<213> Mouse

<400> 134

atgacgcgga	cccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccaaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccaagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttc	gtgtgctgcc	ccagggtctg	240
aaggtaagg	aggtggaggc	cgaggatgcc	ggtggttatg	tgtgcaaggc	ccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg			340

<210> 135

<211> 113

<212> PRT

<213> Mouse

<400> 135

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15

Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30

Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45

Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60

Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80

Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95

Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110

Met

<210> 136

<211> 148

<212> DNA

<213> Mouse

<400> 136

atgacgcgga	cccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagatg	atattagtcc	aggaaaggag	agccctgggc	caggtggttc	ttcggggggc	120
caggaggacc	cagccagcca	gcagtggg				148

<210> 137

<211> 49

<212> PRT

<213> Mouse

<400> 137

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
 20 25 30
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
 35 40 45
 Trp

<210> 138
 <211> 352
 <212> DNA
 <213> Mouse

<400> 138
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgctc ggctgaggcg 60
 gcgcgagcac ggcctcgctt cacacagccc tccaagatga ggcgcccagt gattgcacgg 120
 cctgtggta gctctgtcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttcaa gaaccttgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccgggtgc catcaacgccc acctacaaag tggatgtaat cc 352

<210> 139
 <211> 117
 <212> PRT
 <213> Mouse

<400> 139

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile
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<210> 140
 <211> 421
 <212> DNA
 <213> Mouse

<400> 140
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 gtggacttcg gtgggacaac gtccttccag tgcaaggtgc gcagtgcacgt gaaggctgtg 180
 atccagtggc tgaagcgggt ggagttacggc tccgagggac gcccacaactc caccattgtatc 240
 gtgggtggcc agaagtttgtt ggtgttggcc acgggttgatc tgggttcacg gcctgtatggc 300

tcctaccta acaagctgct catctctcg gccccccagg atgatgctgg catgtacatc 360
tgccctaggta caaataccat gggctacagt ttccgttagcg ctttcctcac tgtattacca 420
9 421

<210> 141
<211> 140
<212> PRT
<213> Mouse

<400> 141
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Glu Arg Thr Arg Ser Lys Pro Val Leu Thr
20 25 30
Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
35 40 45
Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu
50 55 60
Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
65 70 75 80
Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
85 90 95
Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
100 105 110
Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
115 120 125
Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
130 135 140

<210> 142
<211> 67
<212> DNA
<213> Mouse

<400> 142
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gcgcgag 67

<210> 143
<211> 22
<212> PRT
<213> Mouse

<400> 143
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg
20

<210> 144
<211> 1389
<212> DNA
<213> Mouse

<400> 144
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gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctggc 120

cgcactgtgc ggctacagtgc	180
aaagatggcc gcacaatcca	240
aaggtaagg aggtggaggc	300
tttggcagcc tcagcgtcaa	360
acgcacatctag aggctagtga	420
aaggcctgaag acagtggcaa	480
gccacactaca aagtggatgt	540
caccctgtga acacaacggc	600
agtgacgtga agcctgtgat	660
cacaactcca ccattgatgt	720
tggtcacggc ctgatggctc	780
gatgctggca tgtacacctg	840
ttcctcaactg tattaccaga	900
tccacaagcc tgccatggcc	960
ggcactgtgc tgctctggct	1020
cttcctgtgc ctggcgtatcg	1080
ctggccctat tggctgtggg	1140
atcctggcct ctggctcaac	1200
cacacacaca cacatacaca	1260
tcaacaccag catgtccact	1320
gaggtaggca tatgggggcc	1380
gtatcttag	1389

<210> 145

<211> 462

<212> PRT

<213> Mouse

<400> 145

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
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Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20 25 30	
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
35 40 45	
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg	
50 55 60	
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu	
65 70 75 80	
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys	
85 90 95	
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Met	
100 105 110	
Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His	
115 120 125	
Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp	
130 135 140	
Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn	
145 150 155 160	
Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val	
165 170 175	
Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr	
180 185 190	
Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln	
195 200 205	
Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr	
210 215 220	

Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val
225 230 235 240
Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg
245 250 255
Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr
260 265 270
Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro
275 280 285
Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Thr Ser Leu
290 295 300
Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu
305 310 315 320
Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala
325 330 335
Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser
340 345 350
Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile
355 360 365
Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser
370 375 380
Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val
385 390 395 400
His Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly
405 410 415
Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr
420 425 430
Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg
435 440 445
Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser
450 455 460